## STIC-Biotech/ChemLib

From: Sent:

Slobodyansky, Elizabeth Thursday, June 27, 2002 11:35 AM STIC-Biotech/ChemLib 09/801,852

Subject:

Please search for case 09/801,852:

SEQ ID NOs: 1 and 3 against commercial and interference databases.

Thank you.

Elizabeth Slobodyansky, PhD

**Primary Examiner** 

Art Unit 1652 CM1 10D11 703-306-3222

mail box 10C01

POINT OF CONTACT: PAUL SCHULWITZ TECHNICAL INFO. SPECIALIST CM1 6B06 TEL. (703) 305-1954

Searcher:
Phone:
Location:
Date Picked Up:6/28
Date Completed: 7/1
Searcher Prep/Review:/O_
Clerical:
Online time: //>

TYPE OF SEARCH:
NA Sequences: 2
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

VENDOR/COST(where applic.)
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.:
WWW/Internet:
Other (specify):

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nucleic acid
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US-08-932-376A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-932-376A-3
                                                                                                       June 29, 2002, 15:06:19; Search time 135.69 Seconds (without alignments) 4018.766 Million cell updates/sec
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Sequence 11, P
Sequence 6, Ap
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2: /cgn2_6/ptodata/2/lna/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/lna/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/lna/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/lna/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/lna/PCTUS_COMB.seq:*
                    Compugen Ltd
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-09-372-422A-39
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US-09-178-252-26
GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                               383533 seqs, 122816752 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                         nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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2220
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Maximum DB seq length: 200000000
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Match Length DB
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APPLICANT: POILTING, Michael
APPLICANT: Tonzi, Sean M.
APPLICANT: Usher, John J.
APPLICANT: Usher, John J.
APPLICANT: Burnert k, William V.
APPLICANT: Romancik, Guna
TITLE OF INVENTION: REPHALOSPORIN ESTERASE GENE FROM
TITLE OF INVENTION: RHODOSPORIDIUM TORULOIDES
CORRESPONDENCE: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Bristol-Myers Squibb Company
STREET: Rt. 206 & Provinceline Road
CITY: Princeton
STATE: New Jersey
COUNTRY: USA
ZIP: 0854-4000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION: VERSION: 41.30
FLING DATE: 17-SEP-1997
STELING DATE: 17-SEP-1997
STELING DATE: 17-SEP-1997
STELING DATE: 17-SEP-1997
STELING DATE: 17-SEP-1997
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                     US-09-165-264-14
US-08-608-241-5
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US-08-195-264-13
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US-08-165-264-13
US-08-165-264-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: SAVILSKY, Thomas R.
REGISTRATION NUMBER: 31,661
REFERENCE/DOCKET NUMBER: 000144a
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 252-4956
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/08932376A Patent No. 5869309 GENERAL INFORMATION:
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2161 CGTTGTATCGGCCATTCGTGCGTGTAGCTCACTCGAGTATAGACGTTGGCAAGTGCGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1738;
                                                                                                                     APPLICANT: TONZI, Sean M.
APPLICANT: Usher, John J.
APPLICANT: Burnett k, William V.
APPLICANT: Romancik, Guna
TITLE OF INVENTION: REPHALOSPORIN ESTERASE GENE FROM
TITLE OF INVENTION: RHODOSPORIDIUM TORULOIDES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPRENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/932,376A
FILING DATE: 17-SEP-1997
CLASSIFICATION: 435
ATTONET/AGENT INFORMATION:
NAME: SAVITSKY, Thomas R.
REGISTRATION NUMBER: 31,661
REGISTRATION NUMBER: 31,661
REGISTRATION NUMBER: 31,661
TELECOMUNICATION INFORMATION:
TELEPHONE: (609) 252-4956
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1738 base pairs
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                  ADDRESSEE: Bristol-Myers Squibb Company
STREET: Rt. 206 & Provinceline Road
CITY: Princeton
                                                                   Sequence 1, Application US/08932376A Patent No. 5869309
                                                                                              GENERAL INFORMATION:
APPLICANT: Politino, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cuery Match 61.9%;
Best Local Similarity 84.7%;
Matches 1738; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11..1726
                                                                                                                                                                                                                                                                            New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY:
; LOCATION:
US-08-932-376A-1
                                         SULT 2
-08-932-376A-1
                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94 09272
FILING DATE: 25-JUL.1994
PRIOR APPLICATION DATA: WO PCI/FR95/00957
FILING DATE: 18-JUL.1995
ATTORNEY/AGENT INFORMATION:
                              JABER: US/08/776,210
24-JAN-1997
                                                                                                                                                                                                                                             387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICAMY: DORNER, F.
APPLICAMY: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FO
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
STREET: 1800 Diagonal Road, Suit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 acgaacgccggcttgcttgaccag 694
                                                                                                                                                                                                                             32,925
                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-521-2297
TELEFAX: 703-685-0573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                547 ACCAACGCTGGTCTGCACGACCAG
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Best Local Similarity 55.7%;
Matches 147; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                       TELES.A. 248425 EMBON
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 1635 base pairs
                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                           NAME: PATCH, Andrew J
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1635 base pai
TYPE: nucleic acid
STRANDEDNESS: single
                                    APPLICATION NUMBER:
FILING DATE: 24-JAN
                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: 11near
MOLECULE TYPE: CDNA
US-08-776-210-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Alexandria STATE: VA
                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
US-08-232-463-14
                                                                                                                                                                                                                                                                                                TELEFAX:
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                                                                                                                                                                                            1243 GGGGAAGCAGTACCGGATCTCGGACGCGCCGTCAAAGGGCAACACCTTCTCTCGCATCTC 1302
                                                                                                                                                                                                                                                                                                                                                   1367
                                                                                                                                                                                                                                                                                                                                                                                     accettactggccgacgttcgactcgggcaagcagctcctttcaacacgacgacgaggg 1986
                                                                                                                                                                                                                                                                                                                                                                                                      cgctcggcggcttcatcgagacgttcaacccgaacaacaacgctgccaacaagaccatca 1926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1548 ACCCTTACTGGCCGACGTTCGACTCGGGCAAGCAGCTCCTCTTCAACACGACGACGAGGG 1607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1668 CGAGCCAGAAGACCAAGTGCGACTTCTGGCGTGGGTCAATCTCGGTGAACGCGGGTCTCT 1727
                                                                                                   1687 ctgacttcccgcttgcccgcagctgcccgacctactggaccgccgaggcgttcggctcgt
                                                                                                                                    1183 GITCGACCGCCTCCTCGCCGGCCTCTTCCCCTACATCACCTCGGAGGAGCGCCAGGCCGT
                                                                                                                                                                                                                                                                                                                                                   -----CIGCCGACCIACTGGACCGCGAGGCGTTCGGCTCGT
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                                  atteactgacgecactatteagaacgacacgateagegaceagtegeagegegteteeea
                                                                 cgcgaagcagtacccgatctccgacgcgccgtcaaagggcaacaccttctctcgcatctc
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Patent No. 5942639
GENERAL INFORMATION:
APPLICANT: ALIBERT, Gilbert
APPLICANT: MOUGOUNGUI, Zephirin
APPLICANT: BOUDEY, Alain
TITLE OF INVENTION: PROCESS FOR PRODUCING FATTY ACIDS OR
TITLE OF INVENTION: DRIVATIVES THEREOF FROM OLEAGINOUS PLANTS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                            1303 GGCCGTCATCGCGGACTCGACCTTCGT------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :: YOUNG & THOMPSON
745 South 23rd Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM PC compatible SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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OPERATING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
US-08-776-210-5
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1116
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437 gaggattgoctcttcctcaatgtcgttgcccccgccggctggcgagggcgacaatctt 496
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                                                                                                                                                                                                                                                                                                        cagtaccgtctcggcagctttggtttcctcgctggccaagccatgaaggactacggtgta
                                                                                                                                                                                                307 GAGGACTGTCTTACCTTAACGTTTTCCGCCCTGCTGGCACCAAGCCTGATGCTAAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                       ggcagcgactttgccgccttcaccaagcacacgggaaccaagatggtcgttgtaaatctc
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Score 64.4; DB 2;
Pred. No. 4.3e-06
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Gaps

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CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/362,525
FILING DATE: 04-JAN-1995
CLASSITCATION: 435
FILING APPLICATION NUMBER: BP 92202080.5
FILING DATE: 08-JUL-1992
FILING DATE: 08-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 92203899.7
FILING DATE: 14-DEC-1992
PRIOR APPLICATION NUMBER: PCT/EP93/01763
FILING DATE: 07-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REGISTRATION NUMBER: 16,773
REGISTRATION NUMBER: 16,773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 213289/T7020(V)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 862-0944
TELEX: 6714667 CUSH
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "lipase"
/gene= "lipB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 40..1731
OTHER INFORMATION: /product- "lipase"
                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                             1100 New York Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Geotrichum candidum
STRAIN: CMICC 335426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: CDNA to MRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 1828 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.8
Best Local Similarity 55.3
Matches 146; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sig_peptide
40..96
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97..1728
        CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) OTHER INFORMATION:
) OTHER INFORMATION:
US-08-362-525-11
                                                        CITY: ....
STATE: D. C.
COUNTRY: U.S.A.
TP: 20005-3918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 cgtcgtcgacctcggctacgcccgctaccaaggctacttgaacgagaccgccggactcta 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 ccgactcgccgccatgctccttaacctcttcaccctcgcctcccttgctgcgacgctcca 123
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2.9%; Score 64.2; DB 1; Length 72
Best Local Similarity 4.3%; Pred. No. 7.6e-06;
Matches 15; Conservative 206; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  304 gacgcacaaggccgtccgcaacgcgactgagtatggaccgatctg 348
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                   30472/114 IMMU
                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE: P91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 11, Application US/08362525
; Patent No. 6027910
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCHREUDER, MAARTEN P.
TOSCHKA, HOLSER Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORNELIS T
                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: KLIS, FRANCISCUS M. APPLICANT: SCHREUDER, MAARTEN APPLICANT: TOSCHKA, HOLSER Y.
                                                                                                                                                                                                                                                                                                                                    FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
FURBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; CLONE: pTZgpt-Fls
US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: 11near IMMEDIATE SOURCE:
                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-362-525-11
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497 cccgiccicgictacaitcacggaggiggciacgccitcggc----gaigcgagcacc 550 551 ggcagcgactttgccgccttcaccaagcacacgggaaccaagatggtcgttgtaaatctc 610 437 gaggattgcctcttcctcaatgtcgttgcccccgccggctcgtgcgagggggacaatctt 496 463 CCCGTCATGGTTTGGATTTACGGTGCCTTTGTGTTTGGTTCTTCTGCTTCTTACCCT 522 403 GAGGACTGTCTTACCTTAACGTTTTCCGCCCCGCTGGCACCAAGCCTGATGCTAAGCTC 462 Gaps ; 9 Length 1828; 2.8%; Score 62.8; DB 3; Length 1 55.3%; Pred. No. 1e-05; tive 0; Mismatches 112; Indels

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Mon Jul

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APPLICANT: Akira ARISAWA et al.
TITLE OF INVENTION: GENE ENCODING A PROTEIN HAVING ASYMMETRIC
TITLE OF INVENTION: HYDROLASE ACTIVITY FOR 4-SUBSTITUTED 1,4-DIHYDROPYRIDINE DITITLE OF INVENTION: ITS EXPRESSION PRODUCT
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., #800
536 ggcgatgcgagcaccggcagcgactttgccgccttcaccaagcacac----ggggaacc 589
                                      427 GGTGGCACCAGCACCTTCCCTCCCGCCCAGATGATCACCAAGAGCATTGCCATGGGCAAG 486
                                                                                                                          590 aagatggtcgttgtaaatctccagtaccgtctcggcagctttggtttcctcgctggccaa
                                                                                                                                                                       547 GAGATCAAGGCCGAGGGCAGTGCCAACGCCGGTTTGAAGGACCAG 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Streptomyces viridosporus
STRAIN: A-914
                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09000016 Patent No. 6143541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
TELECOMONICATION
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: MES-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09,
FILING DATE: January 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2539 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: genomic DNA ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Warren M. Cheek,
REGISTRATION NUMBER: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ...ATION: 338...2539;
; IDENTIFICATION METHOD:
US-09-000-016-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A. ZIP: 20006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER:
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                                                                                                                                                                                                                                                                                                      US-09-000-016-3
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               476 togtgogagggogacaatetteeegteetegtetacatteaeggaggtggetaegeette 535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      367 accaagecegereccaaccrecegrearecreregarerrreseegeegerrreagere 426
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                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: ALIBERT, Gilbert
APPLICANT: MOULGUNGUI, Zephirin
APPLICANT: MOUDEN, Alain
TITLE OF INVENTION: PROCESS FOR PRODUCING FATTY ACIDS OR
TITLE OF INVENTION: DERIVATIVES THEREOF FROM OLEAGINGUS PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 53.4; DB 2; Length 1650;
Pred. No. 0.0015;
0; Mismatches 131; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,210 FILING DATE: 24-JAN-1997 CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: WO PCT/FR95/00957
FILING DATE: 18-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FR 94 09272
FILING DATE: 25-JUL-1994
PRIOR APPLICATION DATA:
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                                                                                                                                              643 ACCAACGCTGGTCTGCACGACCAG 666
                                                                                                     671 acgaacgccggcttgcttgaccag 694
                                                                                                                                                                                                                                                         Sequence 6, Application US/08776210 Patent No. 5942659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  745 South 23rd Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32,925
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TELEPHONE: 703-521-2297
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Best Local Similarity 51.9%;
Matches 148; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-776-210-6
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1548 cggaggagggccaggccgtcgcgaagcagtacccgatctccgacgccgccgtcaaagggca 1607 1; DB 3; Length 2539; Query Match 2.4%; Score 53.2; DB 3; Length 2 Best Local Similarity 49.1%; Pred. No. 0.002; Matches 168; Conservative 0; Mismatches 173; Indels

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: ROOT-SPECIFIC OR ROOT-ABUNDANT GENE EXPRESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1484 GACGACAAGGACAAGCTCGCCGACTTCTCCTCCACCGGCCCCCGCCTCGGCGACGGCGCC
                                                                                                                                                                                                                                               Length 2809;
                                                                                                                                                                                                                                                  Score 53.2; DB 3; Length 2 Pred. No. 0.002; 0; Mismatches 173; Indels
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SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: A BRASSICA REGULATOR TITLE OF INVENTION: ROOT-SPECIFIC OR ROO NUMBER OF SEQUENCES: 5 CORRESPONDENCE ADDRESS: ADDRESSE: MANDRESSE: MANDRESSE: SOO W. MADISON St. 34th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/915,246
FILING DATE: 19920716
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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Fallis, Lynne
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REFERENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INFORMATION:
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NAME: Pochopien, Donald J.
REGISTRATION NUMBER: 32,16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bellmare, Guy
APPLICANT: Bolvin, Rodolphe
                                                                                                                                                                                                                                                  Query Match 2.4%;
Best Local Similarity 49.1%;
Matches 168; Conservative
                                                                                                                                     ; LOCATION: 2540...2809
; IDENTIFICATION METHOD:
US-09-000-016-1
                                          LOCATION: 338...2539
IDENTIFICATION METHOD:
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STATE: Illino
                                                                                                             NAME/KEY: CDS
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                     NAME/KEY:
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                                                                                          FEATURE:
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TITLE OF INVENTION: GENE ENCODING A PROTEIN HAVING ASYMMETRIC
TITLE OF INVENTION: HYDROLASE ACTIVITY FOR 4-SUBSTITUTED 1,4-DIHYDROPYRIDINE DERIV
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                          1608 acaccttetetegeateteggeegteategeggaetegacttegtgtgegtteeeegte 1667
                                                                                                                                                                                                                        1728 gecgaggegtteggetegteegeeeaaagggeetettegaetaegegeeggeteaeeae 1787
                                                                                                                                                                                                                                                                       1544 ATCAAGCCGGACGTCACCGCTCCCGGCGTGGACATCACGGCCGCCTCGGCGGAGGCAAC 1603
                                                                                                                                                                                                                                                                                                                                                          1604 GACATCGCCCAGGAGGTCGGTGAGGGACCGGCCTACATGACCATCTCCGGCACGTCG 1663
1425 GCCGGGAGTCGATCGCTTCGCCCGCAGCGCGGAGCCCCCCCTCACGTCG-GCGCCGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     1664 Arggcgacccgcacarcacacacacacacacacarcraaa 1705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P. STREET: 2033 K Street, N.W., #800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Diskette, 3.5 inch, 1.44 COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS
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ORIGINAL SOURCE:
ORGANISM: Streptomyces antibioticus
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ORIGINAL SOURCE:
ORGANISM: Streptomyces viridosporus
STRAIN: A-914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/000,016
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Patent No. 6143541
GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 202-721-8200
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SEQUENCE CHARACTERISTICS:
LENGTH: 2809 base pairs
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STRANDEDNESS: double
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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STATE: D.C.
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NAME/KEY: CDS
LOCATION: 19..10722
LOCATION: /codon_start= 19
OTHER INFORMATION: /function="gene erya"
OTHER INFORMATION: /function="gene erya"
OTHER INFORMATION: /function="erya ORF2 encoding modules 3 & 4 for OTHER INFORMATION: 6-deoxyerythronolide B"
FEATURE: NAME/KEY: misc_feature
LOCATION: 19..470
OTHER INFORMATION: /function="approximate span of other information: module 3"
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COCATION: 97.1482
COTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacyl ACP synthase of module 3"
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LCCATION: 3406..3921
OTHER INFORMATION: /function- "approximate span of
OTHER INFORMATION: beta-ketoreductase domain of module 3"
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COCATION: 1693..2671
COCHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain module 3"
               Laboratories D377/AP6D-2 One Abbott
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LOCATION: 4171..428
LOCATION: 4170..428
COTHER INFORMATION: Acyl carrier domain of module 3'
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OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: module 4"
                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/642,734C
FILING DATE: 17-JAN-91
CLASSIFICATION: 435
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ORGANISM: Saccharopolyspora erythraea
STRAIN: NRRL 238
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ATORNEY/AGENT INFORMATION:
NAME: Danckers, Andreas M
REGISTRATION NUMBER: 32652
REFERENCE/DOCKET NUMBER: 495:
TELECHONE: 708-9396
TELEPHONE: 708-9396
TELEPHONE: 708-9396
TELEPHONE: 708-9396
TELEPAX: 708-9396
TELEPAX: 208-9396

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                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
          STREET: Abbott Lak
STREET: Park Rd
CITY: Abbott Park
                                                                                                      CITY: Abbott Park
STATE: IL
COUNTRY: US
ZIP: 60064-3500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1862 oggogogotoggogottoatogagacgttoaacoogaacaacaacgctgccaacaagac 1921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           870 CGCTTCCACCCCCATAACCAGATCCTCCAGGACCACCACCACCACCACCACCAGCAC 811
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
US-07-642-734C-3/C
Sequence 3, Application US/07642734C
Sequence 3, Application US/07642734C
Sequence 3, Application US/07642734C
Sequence 3, Application Security Sequence 3, APPLICANT: Ratz, L
APPLICANT: Moalpine, J
TITLE OF INVENTION: Recombinant DNA Method for Producing TITLE OF INVENTION: Erythromycin Analogs
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 51; DB 1; Length 1505;
Pred. No. 0.0054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO
ORIGINAL SOURCE:
ORIGINAL SOURCE:
STRAIN: Westar
DEVELOPMENTAL STAGE: Somatic
US-07-915-246-1
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TELEPHONE: 312 707-8889.
TELEPAK: 312 707-9155
INPORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1505 base pairs
TYPE: MUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.3 Best Local Similarity 45.6 Matches 221; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              690 CAGCA 686
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LOCATION: 4471..5847
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylACPsynhase domain of module"
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LOCATION: 10831..12174
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylACPsynthase domain of modul"
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                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 7165.9216
COTHER INFORMATION: /duction= "approximate span of
OTHER INFORMATION: /dehydratase and encylreductase domains
                                                                                                              NAME/KEY: misc_feature
LOCATION: 6054..7026
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain of module 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: acyltransferase domain of module 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 12379.13350
OTHER INFORMATION: /function- "approximatr span of
OTHER INFORMATION: acyltransferase domain of module
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modules
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LOCATION: 10225..10483
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain of module 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
COGATON: 14857..15114
OTHER INFORMATION: acyl carrier domain of module 5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
LOCATION: 10723..20235
LOCATION: 10723..20235
OTHER INFORMATION: /codon_start= 10723
OTHER INFORMATION: /function="gene =erya"
OTHER INFORMATION: /product="orf3 encoding modules
OTHER INFORMATION: /edecyerythronolide B formatio"
                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
CCGATION: 9433..9984
OTHER INFORMATION: _/function= "approximate span
OTHER INFORMATION: _beta-ketoreductase of module 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
CACATON: 10723.15165
OTHER INFORMATION: __function= "approximate span of
OTHER INFORMATION: module 5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LCGATUN: 14062.14610
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoreductase of module 5"
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LOCATION: 15166.20235
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: module 6"
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LOCATION: 15172..16569
OTHER INFORMATION: /fur
OTHER INFORMATION: beta
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LOCATION: 16768..17721
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18379..18921
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LOCATION:
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Db 17256 CACGACCGAGGAGGAGGTGACCGCGGCGACGGAGATCCGGTCCTCCCACGGGGGAT 17197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17196 CAGCGCGCGCGCGCTTCACCGGGAGCCGCCAACGAGACCATGCCGCCCTTGCCCGCCAG 17137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1898 gaacaacaacgetgecaacaagaccateaacettaetggeegaegttegaetegggeaa 1957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1540 catcacctcggaggagcgccaggccgtcgcgaagcagtacccgatctccgacgcgccgtc 1599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1600 aaagggcaacacettetetegcateteggcegteategegggaetegaeettegtgtgegt 1659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1660 teceeg--tegtetteteegagtatteegetgaetteeegettgeeegeagetgeeegae 1717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1718 ctactggaccgccgaggcgttcggctcgtccgccacaagggcctcttcgactacgcgcc 1777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1778 ggctcaccacgcgaccgaccactcgtactacatcggctccatctggaacggcaagaagtc 1837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1958 gcagotcotottcaacacgacgacgagggacaccotototocgccgacccgcgca 2013
                                                                                                                                                                                                                                                                                                                                                                                    Length 20235;
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US-08-43-009A-3/C
Sequence 3, Application US/08439009A
Sequence 3. Application US/08439009A
Setent No. 6004787
GENERAL INFORMATION:
APPLICANT: Mats, L
APPLICANT: Malpine, J
TILLE OF INVENTION: Method of Directing Biosynthesis of
TITLE OF INVENTION: Specific Polyketides
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Steven F. Weinstock
STREET: Abbott Laboratories D377/AP6D-2 One Abbott
/function= "approximate span of beta-ketoreductase domain of module
                                                                                                                                                                                                                                                                                                                                                                                    Score 49.2; DB 1; Length 2
Pred. No. 0.032;
0; Mismatches 258; Indels
                                                                        NAME/KEY: misc_feature
LOCATION: 1949...19398
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain of module 6"
                                                                                                                                                                                               NAME/KEY: misc_feature

: LOCATION: 19492..20235

: OTHER INFORMATION: /function= "approximate span of

: OTHER INFORMATION: thioesterase domain of module 6"

US-07-642-734C-3
                                                                                                                                                                                                                                                                                                                                                                                    Query Match 2.2%;
Best Local Similarity 45.4%;
Matches 216; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OTHER INFORMATION:
OTHER INFORMATION:
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                                                FEATURE:
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us-09-801-852a-3.rni

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NAME/KEY: misc_feature
LOCATION: 15172..1656
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylACPsynthase domain of modul"
                    NAME/KEY: misc_feature
LOCATION: 7165..9216
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: dehydratase and encylreductase domains m"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 10831..12114
OCHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylACPsynthase domain of modul"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 18379..18921.
OTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: beta-ketoreductase domain of module 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 10723...20235
OTHER INFORMATION: /codon_start= 10723
OTHER INFORMATION: /function= "gene =eryA"
OTHER INFORMATION: /product= "orf3 encoding modules 5 6 OTHER INFORMATION: 6-deoxyerythronolide B formatio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 12379..13350
OTHER INFORMATION: /function= "approximatr span of
OTHER INFORMATION: acyltransferase domain of module 5"
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LCCATION: 19149..19398
COTHER INFORMATION: /function= "approximate span of OTHER INFORMATION: acyl carrier domain of module 6"
FEATURE:
                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 10225..10483
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyl carrier domain of module 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 15166..20235
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: module 6"
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LOCATION: 14062..14610
OTHER INFORMATION: /function="approximate span of
OTHER INFORMATION: beta-ketoreductase of module 5"
                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 9433..984
LOCHER INFORMATION: /Luction= "approximate span
OTHER INFORMATION: /beta-ketoreductase of module 4"
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LOCATION: 14857_15114
OTHER INFORMATION: _function= "approximate span o
OTHER INFORMATION: _acyl carrier domain of module
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 10723..15165
OTHER INFORMATION: /function= "approximate span
OTHER INFORMATION: module 5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
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/function= "gene eryA"
/product= "eryA ORF2 encoding modules 3 & 4 for
6-deoxyerythronolide B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 4471..5847

OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacylaCPsynhase domain of module"
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LOCATION: 97..1482
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoacyl ACP synthase of module 3"
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COCATION: 3406.3921
COTHER INFORMATION: /Lunction= "approximate span of
OTHER INFORMATION: beta-ketoreductase domain of module 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 6054..7026
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain of module 4"
'BATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: 1693..26710
LOCATION: 1693..2670
LOCATER INFORMATION: Acyltransferase domain module 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: 4171..4428
LOCHER INFORMATION: acyl carrier domain of module 3"
OTHER INFORMATION: acyl carrier domain of module 3"
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CLCGATCON: 4471...10722
OTHER INFORMATION: _________________________approximate span of
OTHER INFORMATION: module 4."
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTAMRE: Patentin Release #1.0, Version #1.25
SUGREENT APPLICATION DATA:
FILING DATE: 11-MX-1995
CLASSIFICATION NUMBER: US/08/439,009A
FILING DATE: 11-MX-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CASALCO, Diamne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 4952.US.D1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 20235 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Saccharopolyspora erythraea
STRAIN: NRRL 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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LOCATION: 19..4470
OTHER INFORMATION: /fur
OTHER INFORMATION: modu
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OTHER INFORMATION: /c
OTHER INFORMATION: /F
OTHER INFORMATION: /P
OTHER INFORMATION: /F
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
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HYPOTHETICAL: N
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                                                                                                                                                                                                                                                                                   1540 catcacctcggaggaggagcaggccgtcgcgaagcagtacccgatctccgacgccgtc 1599
                                                                                                                                                                                                                            2; Gaps
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                                                                                                                                                                     Query Match 2.2%; Score 49.2; DB 3; Length 20235; Best Local Similarity 45.4%; Pred. No. 0.032; Matches 216; Conservative 0; Mismatches 258; Indels 2;
LOCATION: 19492...20235

COTHER INFORMATION: /function= "approximate span of profile INFORMATION: thioesterase domain of module 6" US-08-439-0098-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIF: 10020-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720Kb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS DOS 5.0
SOFTWARE: WordPerfect 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: James F. Haley, Jr., Fish & Neave STREET: 1251 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Nakamura, Etsuo
APPLICANT: Tsuzuki, Hiroshige
APPLICANT: Tsuzuki, Hiroshige
APPLICANT: Kitadokoro, Kengo
APPLICANT: Shin, Nasaru
APPLICANT: Teraoka, Hiroshi
TITLE OF INVENTION: No. 5665586el Protease
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUFTWARE. "SOURCE AND STAR. APPLICATION DATA:
APPLICATION NUMBER: US/08/343,428
FILING DATE: 18-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/J93/00592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08343428 Patent No. 5665586 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 49; DB 1; Length 2064;
Pred. No. 0.017;
0; Mismatches 315; Indels
FILING DATE: 30-APR-1993
APPLICATION NUMBER: JAPAN 4-126511
FILING DATE: 19-MAY-1992
ATTONNEY, AGENT INFORMATION:
NAME: HALEY, Jr., James F.
REGISTRATION NUMBER: 27794
REFERENCE/DOCKET NUMBER: SHGN-7
FELECOMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
; TELEPHONE: (212)596-9000
; TELEPHONE: (212)596-9000
; INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             by experiment
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                                                                                                                                                                                                                                                                                                                                                                          Genomic DNA
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Best Local Similarity 44.1
Matches 249; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 359..364
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 378..383
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 435..1505
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -10 signal
                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
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us-09-801-852a-3.rni

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1479 tcagogaccagtcgcagcgcgtctcccagttcgaccgcctctcgccggcctcttcccct 1538
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Pred. No. 0.026;
0; Mismatches 208; Indels
                                                                                           GENERAL INFORMATION:
APPLICANT: HOTLICK, Robert A.
APPLICANT: Damaj, Bassam B.
APPLICANT: Damaj, Bassam B.
APPLICANT: Commaj, Bassam B.
TITLE OF INVENTION: Eukaryotic Cells Stably Expressing General TITLE OF INVENTION: From Multiple Transfected Episomes FILE REFERENCE: 1987/1D933051
CURRENT APPLICATION NUMBER: US/09/130,114
CURRENT FILING DATE: 1998-08-06
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FRASESQ for Windows Version 3.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/178,252
CURRENT FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: 60/065,215
EARLIER FILING DATE: 1997-11-12
EARLIER FILING DATE: 1998-03-02
NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 26, Application US/09178252
Patent No. 6218188
                                            Sequence 2, Application US/09130114
Patent No. 5976807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1839 gtctcgtccgtccagtccttc 1859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 2.2'
Best Local Similarity 45.4'
Matches 173; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: EBNA
US-09-130-114-2
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1354 GCTCCGCCGCCGCCGACAGCGCGCGCGCCCACTTCGCCGGTTCCGTCGCCCTCGGCATCC 1413
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                                                                                                                                                                                                                                                                 GENERAL INPORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Broad, Natalie
APPLICANT: Breenhader, Jurg
APPLICANT: Breenhader, Jurg
APPLICANT: Toupet, Christine
APPLICANT: Poupet, Christine
APPLICANT: Poupet, Christine
APPLICANT: Poupet, Christine
APPLICANT: Pospiech, Andreas
TITLE OF INVENTION: Staurosporin Biosynthesis Gene Clusters
FILE REPRENCE: 4-20555/A,PCT
CURRENT APPLICATION NUMBER: US/09/029,603
CURRENT FILING DATE: 1998-03-20
EARLIER APPLICATION NUMBER: PCT/EP96/03643
EARLIER APPLICATION NUMBER: PCT/EP96/03643
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 6085;
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Pred. No. 0.034;
1; Mismatches 112; Indels
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ORGANISM: Streptomyces longisporoflavus
                                                 2053 agaagaccaagtgcgacttctggcg 2077
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Patent No. 6210935
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Best Local Similarity 50.4
Matches 115; Conservative
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LOCATION: (2593)..(4011)
OTHER INFORMATION: ORF
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OTHER INFORMATION: ORF
US-09-029-603-4
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LOCATION: (1747)..(2553)
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Pred. No. 0.036;
0; Mismatches 249; Indels 10;
; SEQ ID NO 26
; LENGTH: 1965
; LENGTH: 1965
; ORGANISM: Artificial Sequence
; FEATURE:
; PEATURE:
; OTHER INCRMATION: Synthetic B.t. toxin gene
US-09-178-252-26
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Best Local Similarity 46.7%;
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Search completed: June 29, 2002, 15:07:14 Job time: 20670 sec

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ď	Title:  Perfect score: 2220 Sequence: 1 ggatccaccgaactctgtcagacgttggcaagtgcgaaa 2220 Scoring table: IDENTITY_NUC Gapop 10.0, Gapext 1.0 Searched: 13736207 seqs, 6748477542 residues Total number of hits satisfying chosen parameters: 27472414 Minimum DB seq length: 00 Maximum Match 0% Maximum Match 100% Listing first 45 summaries	Database : EST:*  1: em_estba:* 2: em_esthum:* 3: em_estmin:* 4: em_estmin:* 5: em_estpin:* 6: em_estpi:* 7: em_estpi:* 10: qb_esti:* 11: qb_htc:* 12: qb_gs:* 13: em_gss_hum:* 15: em_gss_ph:*	16: em_gss_vrt:*  Pred. No. 1s the number of results predicted by chance to have score greater than or equal to the score of the result being and is derived by analysis of the total score distribution.  SUMMARIES  Score Match Length DB ID  Score Match Length DB ID  64.2 2.9 828 12 CNS046HZ 66.5 2.7 793 12 CNS016HZ 59.4 2.7 1101 12 CNS016MU AL10694 59.2 2.7 649 9 AA246278 AA246278 AA246278 AA246278	59.2 2.7 6/3 10 B15/4042   B15/4042 KH018457.5     6 59.2 2.7 6/6 10 B15/4045   B15/4042 KH018457.5     7 58.6 2.6 880 12 CNS04463   AL273684 Tetracadon c 10 58.4 2.6 925 12 CNS0310   AL533113 Drosophil aL20858   AL273684 Tetracadon c 11 58.2 2.6 1463 10 BM320858   Be636746 rockefell c 14 57.6 2.6 1011 12 AG126307   AL562307 Pen trogl c 16 57.2 2.6 568 9 AL572700   AL572700 AL572700 aL572700 c 17 57.2 2.6 873 12 AG136937   AG136937 Pan trogl

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This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
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1 (bases 1 to 793)
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., a Fizames, C., Wincker, P., Brottier, P., Quetler, F.,
Saurin, W. and Weissenbach, J.
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Tetraodon nigroviridis genome survey sequence PUC-Ori end of clo
194C21 of library G from Tetraodon nigroviridis, genomic survey
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/db_xref="taxon:99883"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre & Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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BACN16C14 of DrosBAC library from Drosophila melanogaster (fruit
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                              28
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/clone="lb-"G"
/note="Genoscope sequence ID : COAC
                                                                                                                                                                                                                                                                ; Score 60.6; DB 12;
; Pred. No. 0.7;
14; Mismatches 143;
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BACKSA111 of RPCI-98 library from Drosophila melanogaster (fruit
ALDY), genomic survey sequence.
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Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1101)
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                                      233 others
                                                                                                          Similarity 42.1%; Score 59.8; DB 12; Length Similarity 42.1%; Pred. No. 1; 06; Conservative 30; Mismatches 157; Indels
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                                      185
                                    59 g
/clone="BACN16C14"
/note="end : T7"
525 c 59 g
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/organism="Drosophila melanogaster'

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/note-"Organ: embryo; Vector: BlueScript SK; Site_1: EcoRI ; Site_2: XhoI; Constructed using Stratagene ZAP-cDNA Synthesis Kit. oligo dT-primed and directionally cloned at EcoRI and XhoI is a 176 g 151 t 1 others
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LD02542.5prime LD Drosophila melanogaster embryo BlueScript
Drosophila melanogaster CDNA clone LD02542 5prime, mRNA sequence.
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/clone_llb-"LD Drosophila melanogaster embryo BlueScript"
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/dev_stage="0" to 24 hours mixed stage embryonic"
/lab_host="SOLR"
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 625)
Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 25 row: D column: 6
High quality sequence stop: 484.
Location/Qualiflers
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/db_xref="BDGP_EST:BDc1n002213"
/db_xref="taxon:7227"
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2.7%; Score 59.4; DB 12;
Best Local Similarity 41.2%; Pred. No. 1.2;
Matches 99; Conservative 27; Mismatches 114;
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/clone="BACR34B11"
/note="end : TET3"
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/lab_host="SOLR"
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LD05065.5prime LD Drosophila melanogaster embryo BlueScript
Drosophila melanogaster cDNA clone LD05065 5prime, mRNA sequence.
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1 (bases 1 to 649)

Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, Lewis, S. and Rubin, G.M.

BDGP/HHMI Drosophila EST Project
Unpublished (2001)
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Plate: 50 row: F column: 5
High quality sequence stop: 539.
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tive 0; Mismatches 78; Indels
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/organism="Drosophila melanogaster'
                                 78;
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One Cyclotron Rd, Berkeley, CA 94720, USA
Pax: 510 486 6798
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 Score 59.2; Di
Pred. No. 1.2;
0; Mismatches
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59.28;
Query Match 2.7
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Matches 122; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryofera, Metazoa, Arthropoda, Tracheata; Hexapoda, Insecta;
Pterygota; Neoptera: Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

[ (bases 1 to 673)
Stapleton,M., Brokstein,P., Hong,L., Tyler,D., Berman,B., Carlson,J., Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E., George,R., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G., Misra,S., Phouanenavong,S., Wan,K., Yu,C., Lewis,S.E., Celniker,S. and Rubin
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BamHI: Library was Kindly generated by Piero Carnincl at
the RIKEN. The library was normalized and excised using
Ce recombinase. Plasmid cDNA library."
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/organism="brosophila melanogaster"
/db_xref="taxon:7227"
/clone="RH09457"
/clone_lib="RH Drosophila melanogaster normalized Head
434 toggaggattgcctcttcctcatgtcgttgccccgccggctcgtgcgagggcgacaat 493
                                                                                                                        Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Eax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003454: arm:2R [16312727,16613591]
estimated-cyto:57011-5788: 07/26/2001
Plate: RH.94 row: E column: 9
High quality sequence stop: 577.
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Best Local Similarity 59.2%; Pred. No. 1.2;
Matches 122; Conservative 0; Mismatches 78;
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/lab_host="DH5-alpha TonA"
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                                                                                                                                                                                                                                          614 taccgtctcggcagctttggtttcct 639
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Other_ESTs: RH09457.3prime
Contact: Stapleton, M.
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Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                     CNSO4463 880 bp DNA linear GSS 18-MAY-2000 Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 080P10 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL273684
AL273684.1 GI:7995946
AL273684.1 GI:7995946
GSS; genome survey sequence.
GSS; genome survey sequence.
Tetracdon njgroviridis.
Tetracdon njgroviridis
Tetracdon njgroviridis
Acathopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acathomorpha; Acanthopterygii; Percomorpha; Tetracdontiformes;
Tetracdontidae; Tetracdon.
1 (bases 1 to 880)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence Unpublished
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Roest-Crollius.H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottler,P., Quetier,F.,
Saurin,W. and Welssenbach,J.
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                                                                                                                                           494 TICCACTITCCCG-----CCAAGCICATGGAGCAGGAGGICATIGIGGTCACCCTGAAT 547
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494 cttcccgtcctcgtctacattcacggaggtggctacgccttcggcgatgcgagcaccggc
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/clone="080P10"
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44.0%; Pred. No. 1.6;
ative 18; Mismatches 182;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (2016)
Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B., Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, M., Ghavalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Misra, S., Mungall, C.J., Nunco, J., Pacleb, J., Paraqas, V., Park, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and Rubin
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/lab_host="DH5-alpha TonA"
/lab_host="DH5-alpha TonA"
/note="Organ: head; Vector: pFlc1; Site_1: XhoI; Site_2:
BamHI; Library was kindly generated by Piero Carninci at
the RIKEN. The library was normalized and excised using
the recombinase. Plasmid cDNA library."
159 c 191 g 168 t lothers
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/db_xref="taxon:722"
/db_xref="taxon:722"
/clone="Ref1852"
/clone_lib="RH Drosophila melanogaster normalized Head
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003454: arm:2R [16312727,16613591]
estimated-cyto:57D11-57F8: 08/23/2001
Plate: RH.618 row: E column: 4
High quality sequence stop: 579.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                            554 agcgactttgccgccttcaccaagcacacgggaaccaagatggtcgttgtaaatctccag
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  cttocogtcctcgtctacattcacggaggtggctacgccttcggcgatgcgagcaccggc
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0; Mismatches 78;
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Contact: Stapleton, M.
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Best Local Similarity 59.2%;
Matches 122; Conservative
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BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoryo Oscegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library as prepared by seconstructed by partial EcoxI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://www.individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be
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sequence TET3 end of BAC #
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Pterzygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
I (bases 1 to 923
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125 ctcgcctttgcctctccgacctccctcgtccgccgcacgaacccaaacgagccccctccc
                     262 cedecedecedecedecidexendecedecedecedecedecedeceder
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/db_xref="taxon:7227"
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Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
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GSS; genome survey sequence.
GSS; genome nigroviridis.
Tetracdon nigroviridis.
Tetracdon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetracdontiformes;
Tetracdontidae; Tetracdon.
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetier, F.,
Saurin, W. and Welssenbach, J.
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                                                                                                         799 HSSSSACBSSSSCSASCWSASSSSASSSRSRSGGGGGGGGGGGGSGRSSSSSSSASAGGV 740
739 VSSASSSSSCSSSVSCSSVASSMSCSSBSSSSASASSSSSSSSASCASCCCCTSWSCS 680
                                                                                                                                                                                                                                                                                          303 cgacgcacaaggccgtccgcaacgcgactgagtatggaccgatctgttggccggctagcg 362
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                                                                                                                                                                                                                                                                                                                                                                                                                              243 actggtggcgcggaatccgctacgcctcggctcagcgcttccaggctcctcagacgcccg
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/db_xref="taxon:99883"
/clone="031B04"
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42.6%; Pred. No. 1.7;
tive 34; Mismatches 162;
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Location/Qualifiers
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/note="Genoscope sequence ID
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/strain-"ATCC 30984"
/db_xref="taxon:108607"
/clone_lib-"Mastigamoeba balamuthi lambda ZAP II Library"
/note-"syn: Phreatamoeba balamuthi"
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The Rockefeller University
Email: mmuller@rockvax.rockefeller.edu
Insert Length: 1463 Std Error: 0.00
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Gordon,P., Durufle,L., Gaasterland,T., Lopez,P., Muller,M. and
Philippe,H.
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ccaccogaactotgtcccgctttctggctttcttccttgctgtcgcccatcgcctttcc
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Mastigamoeba balamuthi
Eukaryota; Pelobiontida; Mastigamoebidae; Mastigamoeba.
1 (bases 1 to 1463)
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llarity 44.8%; Pred. No. 2;
Conservative 0; Mismatches 323;
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Lee J.A., Moore D.V., Gordon P., Sensen C.W., Gaasterland T., Muller M.; "CDNA clones (expressed sequence tags) from the free-living amitochondriate amoeboflagellate, Mastigamoeba balamuthi";
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Laboratory of Biochemical Parasitology
The Rockefeller University
1230 York Avenue, New York, NY 10021, Umail: mmuller@rockwax.rockefeller.edu
Insert Length: 1464 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3SS; GSS (genome survey sequence). Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
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Pan troglodytes DNA, clone: PTB-136N06.F, genomic survey sequence.
AG126307
                                                           /clone_lib="Mastigamoeba balamuth1 lambda ZAP II Library"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Direct Submission
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Totoki, Y., Matanabe, H. and Sakaki, Y.
                                                                                                                                                              Score 58; DB 3; Length 1464;
Pred. No. 2.2;
0; Mismatches 240; Indels
                                                                                                  BP; 281 A; 548 C; 382 G; 252 T; 1 other;
/note="syn: Phreatamoeba balamuth1"
    /organism="Mastigamoeba balamuthi"/strain="ATCC 30984"
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Unpublished
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GSS; GSS (genome survey
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Local Similarity 46.9%;
nes 213; Conservative
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Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G., Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
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Pterygota, Neoptera, Endopterygota, Diptera, Brachycera,
Muscomorpha, Ephydroidea, Drosophilidae, Drosophila
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On Mar 16, 1999 this sequence version replaced gi:4419821
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                                                                                                                                                                                                                                                                                                       Length 1011;
                                                                                                                         /sex="male"
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a 74 c 631 g 24 t 120 others
                                                                                                                                                                                                                                                                                                          Score 57.6; DB 12; Length
Pred. No. 2.4;
0; Mismatches 247; Indels
                        1 .1011
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="PTB-136N06.F"
Location/Qualifiers
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Location/Qualifiers

1. .568

/organism="brosophila melanogaster"
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/note="Organ: embryo; Vector: pOT2; Site_1: EcoRI; Site_2: XhOT; Sized fractionated cDNAs were directly ligated into
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htt genomic AE003454: arm:2R [16312727,16613591]
estimated-cyto:57D11-57F8: 04/10/2001
Plate: LD.427 row: B column: 11
High quality sequence stop: 568
POLYA-No.
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                                 Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
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Contact: Stapleton, M. BDGP
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Best Local Similarity 58.8%;
Matches 120; Conservative (
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Search completed: June 29, 2002, 13:05:51 Job time: 13722 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	OM nucleic - nucleic search, using sw model Run on: June 29, 2002, 15:03:51; Search time 7060.77 Seconds (without alignments) 6579.581 Million cell updates/sec	Title: US-09-801-852A-3 Perfect score: 2220 Sequence: 1 ggatccacccgaactctgtcagacgttggcaagtgcgaaa 2220 Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Searched: 1797656 seqs, 10463268293 residues	mber of hits satisfying chosen para DB seq length: 0 DB seq length: 2000000000 cossing: Minimum Match 0% Maximum Match 100%	Database : GenEmbl:*  1: gb_ba:* 2: gb_htg:* 3: gb_ln:* 5: gb_on:* 6: gb_pat:* 7: gb_ph:* 8: gb_ph:*		20: em_on:* 21: em_or:* 22: em_or:* 23: em_pat:* 24: em_ph:* 25: em_pp:* 26: em_ro:* 27: em_sts:* 29: em_un:* 29: em_htg_hum:* 30: em_htg_olum:* 31: em_htg_olum:* 33: em_htg_olum:* 33: em_htg_olum:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.  SUMMARIES  Result  No. Score Match Length DB ID  Description

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Politino,M., Tonzi,S.M., Usher,J.J., Burnett,W.V. and Romancik,G. Cephalosporin esterase gene from Rhodosporidium toruloides
Patent: US 5863309-A 1 09-FEB-1999;
Location/Qualifiers
1. 1738
                    GICICIAGGGGGTCTITCCTTCCGACTTCCTTCGTTCTTTCGTTGTTTATTCTTGCAGTTC 2160
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Sequence 1 from patent US 5869309.
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tgtaacgaacgccggcttgcttgaccaggtgagtttcccgcatgatacccgcccaccttt 726

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1111	Db 1368 CCGCCCACAAGGGCCTCTTCGACTACC  Qy 1807 acatcggctccatctggaacggcaag  111111111111111111111111111	RESULT 5 BD005938 LOCUS DEFINITION Cephalosporin esterase gf ACCESSION BD005938 VERSION BD005938.1 GI:18634309 KEYWORDS TP 2001501466-A/1. SOURCE Unidentified ORGANISM Unidentified Unclassified. REFERENCE I (bases 1 to 1738) AUTHORS POlltino, M., Tonzi, S.M., TITLE Cephalosporin esterase gf TITLE Cephalosporin esterase gf TITLE PATORI 19 2001501466-A.	COMMENT OS Unidentified  PD 06-FEB-2001  PF 11-SEP-1997 JP 1998  PR 18-SEP-1997 JP 1998  CC TOPOLOGY: Linear;	FEATURES 1. Docation/Qualification/Qualification/Conganism="unide to the control of the control	Query Match Best Local Similarity 84.7%; Property Partners 1738; Conservative 0; Qy 67 actcgccgccatgctccttaacctct
	TGTAACGAACGCCGGCTTGAC	1087 cgacaaactgcaccaaagccgcctcgtccttcgcttgcctcgaagctgtcgacgtgcggg	1327 gtcgaccggctcgcagaacctcttcaccgggatcaacaacctcgacgaagatgagttccc   138	1507 gttcgaccgcctcctcgccggcctcttcccctacatcacctcggaggagcgccaggccgt 1   1183 gttcgaccgcctcctcgccggcctcttcccctacatcacctcggaggagcgccaggccgt 1   1183 gttcGaccgccTcTcCCCTACCCCTACCTCGGAGGAGGAGGCGCGCTTCTCCCTACCTCGGAGGAGGAGGAGGCGCGCTTCTCCCTACCTCGAGGCAGGAGGAGGAGGAGGCGGT 1   1567 cgcgaagcagtacccgatctccgacgccgtcaaagggcaacacacttctctcgcatctc 1   1184	1627 ggccgtcatcgcggactcgtcgtgtgcgttccccgtcgtcttctccgagtattccg 1303 GGCCGTCATCGGACTTCGT  1303 GGCCGTCATCGGACTTCGT  1687 ctgacttcccgcttgcccgcagctgcccgactactggaccgcgaggggttcggctcgt  111111111111111111111111

2 1738 bp DNA linear PAT 31-JAN-2002 gene from Rhodosporidium toruloides. 18514766 60/026929 SEAN M TONZI,JOHN J USHER,WILLIAM V BURNETT, catcgttgagacttcaagcttgaccgacttggca 2046 ctggcgtgggtcaatctcggtgaacgcgggtctct 2106 , Usher,J.J., Burnett,W.V. and Romanc,G. gene from Rhodosporidium toruloides SGCGCCGGCTCACCACGCGACCGACACTCGTACT 1427 itteaccttggcttcctgctgcgacgttccagt 126 gtccgccgcacgaaccaaacgagcccctcccgt 186 core 1375; DB 6; Length 1738; red. No. 3.6e-203; Mismatches 0; Indels 313; Gaps , C12N9/16, C12N15/00 cation/Qualifiers .1726. 328 t identified" on:32644" 444 g 328

Oy 1267 agaagaacctcaatggcgtgcgtg   1065	Qy         1447 attcactgacgccactattcagaa	567 cgcgaagcagt 11111111 243 CGCGAAGCAGT 627 ggccgtcatcg 111111111111111111111111111111111111	1687 ctgacttcccgcttgcccgcag 1330	1807 acatcsgctccatctggaa 	1927 accettactggccgacgt 	66 10 72	RESULT 6 AF025410 LOCUS DOCUS DEFINITION Rhodosporidium toruloi COMPLETE cds. ACCESSION AF025410 VERSION KEYWORDS SOURCE Rhodosporidium toruloi ORGANISM Rhodosporidium toruloi ORGANISM Rhodosporidium toruloi BUXATYPOTA BUXATYPOTA Microbotiyomycetidae;
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qa	1082	AACCTCTTCACGGGATCAACAACTCGACGAAG
δy	1387	cgacggctctgttcgcccagcgagactgacttgttcttttgcgaagattacgattcat 144
QO	1116	ATTCA
QY	1447	attcactgacgccactattcagaacgacacgatcagcgaccagtcgcagcgcgctctccca 1506
qa	1123	CAGCGCGTCTCCC
ΟŊ	1507	gttcgaccgcctcctcgccggcctcttcccctacatcacctcggaggagcgccaggccgt 1566
đ	1183	TTGACCGCCTCTTCGCCGGCCTCTTCCCCTACATCACCTCGGAGGAGCGCCCCA
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QΩ	1243	GCGAAGCAGTACCCGATCTCCGACGCGCCGTCAAAGGGCAACACCTTCTCTCGCAT
ΟY	1627	gttccccgtcgtcttctccga
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đ	1368	GCCCACAGGGCCTCTTCGACTACGCGCCGGCTCACCGCGACGCGACAACTCGTA
οy	1807	acatogotecatetggaacggcaagaagtcggtetegtecatecagtecttogacggcg 1866
qa	1428	carcescricissacescaaeacescaescescricescescearcericaeses
Qy	1867	cgctcggcggcttcatcgagacgttcaacccgaacaacgaccacaacaagaccatca 1926
đ	1488	SCICGGCGGCTICATCGAGGTTCAACCGAACAACAAGGCTGCCAACAAGACCAT
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qa	1668	SCCAGAAGACCAAGTGGGTTTCTGGCGTGAATCTCGGTGAACGGGG
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GSSAHKGLFDYAPHATDMSYTGIWWKKKSVSYQSFDGALGGFIETFNDNNNA
NKTINDYWPTFDSGKQLLFNTTTRDTLSPADPRIVETSSLTDFGTSQKTKCDFWHGSI
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Politino,M., Tonzi,S.M., Burnett,W.V., Romancik,G. and
Purification and characterization of a cephalosporin es
                                                          Rhodosporidium toruloides
Appl. Environ. Microbiol. 63 (12), 4807-4811 (1997)
                                                                                                                (bases 1 to 1738)
Tonal,S.M., Burnett,W.V. and Politino,M.
Tonal,S.E.C. Submission
Submitted (15-SEP-1997) Biotechnology Development
Bristol-Myers Squibb Co., 6000 Thompson Road, E. S
                                                                                                                                                                                                                                                                             toruloides
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Pred. No. 6.4e-203;
0; Mismatches 1;
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Homo sapiens chromosome 16 clone RP11-47311, WORKING DRAFT
SEQUENCE, 28 unordered pleces.
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Catarrhini; Hominidae; Homo.
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Consensus quality: 126903 bases at least Q30
Consensus quality: 135461 bases at least Q30
Estimated insert size: 138300; agarose-fp estimation
Estimated insert size: 162856; sum-of-contigs estimation
Quality coverage: 5.37 in Q20 bases; agarose-fp estimation

* NOTE: This is a 'working draft' sequence. It currently

* consists of 28 contigs. The true order of the pieces
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN
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Center clone name: RPCI-11_47311
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Eukaryota; Metazoa; Chordata;
Mammalla; Eutherla; Primates;
1 (bases 1 to 16556)
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2 (bases 1 to 165556)
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Consensus quality: 175579 bases at least Q30
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Consensus quality: 186449 bases at least Q30
Consensus quality: 186449 bases at least Q30
Estimated insert size: 198300; squore-ofp estimation
Estimated insert size: 293091; sum-of-contigs estimation
Quality coverage: 3.28 in Q20 bases; squore-off estimation
* NOTE: This is a "working draft" sequence. It currently
* consists of 101 contigs. The true order of the places
* is not known and their order in this sequence record is
* arbitrary. Gaps between the confliss are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                      AC084799 303091 bp DNA linear HTG 17-NOV-2000 Mus musculus chromosome 16 clone RP23-197M9, WORKING DRAFT SEQUENCE, 101 unordered pieces.
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Submitted (17-NOV-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Center: Joint Genome Institute
Center: Joint Genome Institute
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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Unpublished
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Center Project Name: 0
Center clone name: RPCI-23_197M9
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57024 CCCCCCCCCCCCCNNNCCCCCNNNCCCCC 56992 

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3.2%; Score 71.8; DB 2; Length 220469;
Best Local Similarity 22.3%; Pred. No. 0.024;
Matches 250; Conservative 0; Mismatches 873; Indels 0;
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    /organism="Mus musculus"

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220469 bp DNA 11near HTG 26-JUL-2000 Mus musculus chromosome 16 clone RP23-6K21, WORKING DRAFT SEQUENCE, 42 unordered pieces.
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DOE Joint Genome Institute.
Sequencing of Mouse
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Consensus quality: 179034 bases at least Q30
Consensus quality: 187032 bases at least Q30
Consensus quality: 187032 bases at least Q30
Estimated insert size: 216360; aganose-fp estimation
Estimated insert size: 216369; sum-of-contigs estimation
Quality coverage: 3.09 in Q20 bases; agarose-fp estimation

* NOTE: This 1s a "overking draft' sequence. It currently

* consists of 42 contigs. The true order of the pieces

* is not known and their order in this sequence record is
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Consensus quality: 140511 bases at least Q40
Consensus quality: 156778 bases at least Q30
Consensus quality: 156778 bases at least Q30
Consensus quality: 156778 bases at least Q30
Consensus quality: 164746 bases at least Q30
Estimated insert size: 180188; sum-of-contigs estimation
Estimated insert size: 180188; sum-of-contigs estimation
Quality coverage: 3.83 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
consists of 19 contigs. The true order of the places
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                        AC090552 181988 bp DNA 11near HTG 01-AUG-2001
Homo sapiens chromosome 3 clone RP11-759M11, WORKING DRAFT
SEQUENCE, 19 unordered pieces.
                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 181988)
DoE Joint Genome Institute.
Direct Submission
Submitted (03-MAR-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA on Apr 25, 2001 this sequence version replaced gi:13194218.
                                                                                                                                                                                             Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 181988)
Dos Joint Genome Institute.
Sequencing of Human Chromosome 3
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1472: gap of unknown length
2486: contig of 1014 bp in length
4020: contig of 1434 bp in length
4120: gap of unknown length
5514: contig of 1294 bp in length
5514: contig of 1294 bp in length
6649: contig of 1185 bp in length
6749: gap of unknown length
6749: gap of unknown length
6749: contig of 1147 bp in length
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contig of 2083 b
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gap of unknown
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Center Project Name: 0
Center clone name: RPCI-11_759Ml1
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Center Code: JGI
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AC090552.2 GI:13786433
HTG; HTGS_PHASE1; HTGS_DRAFT.
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of 54796 bp in length.
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unknown length
of 6803 bp in length
unknown length
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/clone="RP11-759M11"
/clone=11b="RPCI human BAC library 11"
1 36221 c 36728 g 51237 t 4580 oth
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Pred. No. 0.051;
0; Mismatches 894;

    181988
    /organism="Homo sapiens"
    /db_xref="taxon:9606"

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The orientation of the sequence is from SP6 to T7 of the PAC clone. Genes were predicted from the integrated results of the following:GENSCANI.0, BLASTAZ.0 as well as following:GENSCANI.0, BLASTAZ.0 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against the non-redundant database NRP (PIR, SWISSPROT, GENPEPT, PDB) from MAFF DNA bank and the cDNA sequence database at RGP. Protein similarities of the coding regions were searched against NRP with BLASTP2.0. ESTS represent the identified cDNA sequences using BLASTP2.0 with the corresponding DDBJ accession no. This sequence of this clone has an overlap with P0541H01 clone, DDBJ.AP001389 at the 3' end.

This clone ends at the position 26,826 of P0541H01. Detailed information on overlap and assembly quality together with annotation of this entry at http://www.dna.affrc.go.jp:82/genomicdata/GenomeFinished.html.
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Oryza Bativa geneomic DNA, chromosome 6, PAC clone:P0029D06.
AP001552
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Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza
1 (bases 1 to 150120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (29-MAR-2000) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (Emali:tsasaki@abr.affrc.go.jp, URL:http://www.dna.affrc.go.jp, Fax:81-298-38-7441,
                                                                                                                                                                                                                                                                                                                                                                                  caaggeteteggteteaagaageeeetetteeaegetgeeateggeteeteegtetteet 1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cccctaccaagccaagtacaactccccttcgccgagctgctctactcccaactcgtctc 1084
                                               ttcgactcatgctgacgcctctcccgctcgcagcaattcgcccttcaatgggttcaacag 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6, PAC
                                                                                                                                                                                                                                                     845 gcagggtccgttatgaaccagatcattgcgaacgtgagccacccgaaccgatctccagcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cacgtctcgaagttcggcggcaaccccgatcacgttacgatttggggcgagtctgcaggc
                                                                                                                                                                                                                                                                                                                                                       gactttcccccccccccccccccgctgacctccctcgtcttgcagggcggcaaccgt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (cultivar:Nipponbare) DNA, clone:P0029D06
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome
clone:P0029D06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2108 CNCCCCCNCCCCCCCCCCCCCCCCCCCCNNNNCCNNNNC 2061
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SOURCE
ORGANISM
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TITLE
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AUTHORS
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complement(join(29217. 30334,31321. 31609,31701. 31862))
/note="hypothetical protein"
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GYTNEFSNSLOKROQDIVNAMSLVGLAKKMOOMRFNGHERSFEEVFEVNAHLALVIL
GYTNEFSNSLOKROGDIVNAMSLVGLAKKKMOOMRFNGHEGFLGKVTSFCIKYSIDIP
AMDAKYVPHGRSHRYVPYQTIDDHYRREVYIGVIERHQGLENRFDBYSMELLLCMSA
FNPTDSFASFDAQKILKLASFYPKDIEGSNLMKLELQLDTYINDMREDHRFKGLNKIG
QLSIKLWPTKHDLYPDLYYLLKLVVLLLDVATASVERVFSAMNLVKTKVRNSMSDKLL
NNCLYTFIERDMYMRKT"
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LLAFTGTCHSWRAAFSSYPSKSNFRIILPPLLVRPNVRVKAPYSSNGHRKLRSCEVID
LLANRNPPLRCQIPGTLORMHPAGSSHGQLICCRRGYCLVVDVFTGARSVBPRLLEFSE
NCDBFYVCGILTAPITSPNSHLIISTGSSLFDWPVGSDSWEELFVNRVQQYBFNG
QLIAVIESYLYTLQAFILERLEKIKTLMWDNMRCPYNRRWFVVCGDMLLIVDHYISF
SFGAPVLXRPYRLDMSTKPAKWVEVKKLENWALFIGGDARSPPFSFKNPERRGGRSNC
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LFFETACRLLKPDSFILSAAFHLYEHSGRESEAGDVLDAINMSGASFLRNLKVGSKLE
                                                                                                                                                                                                                    QKQVIRCCSMETTSCILKELGDEHYAILADESSDISHKEQLVVCLRYVDKLGGVCERF
LAVVHVAGTSSLQLKTAIQSLLTSHHLTLTQIHGGYDGASNMKGEVKGKCWLPNLFG
QVSRLLNIVGVSCTRHDMLRDVRAQKLKKALNLGEIASGSGLNQEMALARPGDTRWGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MYQIKIKKKRDEVLVATRLGEKVESLQALRMDGRVSGDDDAGE
RRPLRRCRRAQCGPKSKVGLDWLGLPWIITSLTHPPPRLASTPIGRAAAAAAVATAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IALLSSEQDLLAFSGTCRSWRAALSSFPSIYTFTFPPLHLKPDIPNSHPHCSSFRYTL
LYKCRWQLGDPSKRTLSLRCSAPQNTPNRMRYLGCSYGYLIFSYYENCLLVDMYTGAK
VKPPKLQSAGNKETYYGILTAPLNLFISHLLCSRSSIFYWQVGTNSWSEHPFGGERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LQIVLFKGEFFAMDFHHRLHTWRFAPQLSMQEVGVVWGEEMFVGVHFKPWLVISGDML
LMLDLSVGIHHSYGFPGTFQVFRLDFSAQTAKWMKMEKLENSALFVSLDRRNPTFSCT
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38724. .39212)

/note-"Similar to Arabidopsis thaliana DNA chrmosome V, BAC clone TWO21804; N. tabacum membrane-associated
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/db_xref="G1:7363277"
/tb_xref="G1:7363277"
/translation="WAAAIAGAAASTAVSITCSSYSYEDDGAATSWSLSSGTSSSSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QIQPKWWSIVKSGPLFPQKAHGVPLKYKQRSPWCCSVEQVVAREGEVDAAQRFGSRDA
AVHDHVQRYDSSTCD"
                                           IVVDEGVCEETEEDTVVDDAPPPDVVVDEVSIETKEESLPIYDVDDLEHDPGLRVPIS
SFDANDQDAARRGYILKGPCHLWAFNFPSRKIYGKDRRFSVIWFHKYPWIEYSVDKDA
                                                                                                                             TFCFVCYLEGKESGKFVTGGWHNWNVGAKALDKHVGGTSSDHNFAQEKYNLFVKKGCL
RYLLRQGLAFRGHDETEESNNRGNFLELLKWLAGNNENANKVVLNNAFGNCILTSPRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NPERWGGKSNCIYVAKPSEDSDEPWTAVELGQPIPGATHCVPYSHPLLRTEGHCSQLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSSPAHPGKLRVSKRSWTGAAGSGSGEDHGRRRRRPSPRQRSSPLSAKGLMDSMLHQ1
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/db_xref="GI:7363276"
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/note="3' LTR"
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/krvbvahation="MIKAPIATVLGRSRCLEGLAAGGGRLARHEEA"
/forner="Mypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /proteil_16="BAA93014.1"
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EGEEGVRERASGAGDGASHIFCCSSPPTLLGKSGTPPSGVRGRERESGGIGEMKSM
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TPGPDGHRVRPPPADVTTRRGIRREEAPASGPTDVVCAAMRRRGLMVAAAVPPPPRP
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RGRDAGTWAPLAVAQGGRGCGWQAGPTGHGSKREGAASAGLGSAPSRPAGERRRQAAT
DGGDRREDGDSRRRGRRHIAATRMRGAAARARGREGEGVLTGVRPATREETTTNGDAA
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DIPLPSPPESRRPTLPAASAAAPSRQPPRPASGQRHSISGSGSALRLSGLRI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id-"Baa93013.1"
/db_xref-"G1:7363269"
/translation-"MARRGKDLISQLPDDILLHILSMVRYKBAVRTAAVSRWKHLH
/translation-"MARRGKDLISQLPDDILLHILSMVRYKBAVRTAAVSRRWKHLH
PREPALSFINGVLGAGGSSLSTGSRQRVDSMARTLRRRCAGPDRDTVRLCLAYRKDV
PMEGRYADET ALAAASSLGLFLNCFKULRNDDAGPWSLHLPAATAGLSMESGWYSVR
PPHVHGPGASALKSLTFKDSFWVLHPGYLQDTAFPSLEELHISGCTLSGSIEITSATM
PRLKHLRIADVSVVSLGTAAAIAVLADBLTTLRVSCHDGGKPDPPSSHEMLCVETLFR
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FLOMEDDEKLMNDILLGIMPGRWKYVOSLPYFRARNKYWRWGEODDREEBEVGONHPR
MDMLTTHAASAGFGGDCTAASDGVYMAATARGEDGGNSDRLGSGVMEDLGIGAARWN
RPADRARRERWRPGGGRRGRRGNEAVTGWARRRRAERYSIVTAGGSTSARLRRPDAAR
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SSDAGWAHGRURRKGROGGRVPRAGEHRTMAYTVEGH"
join(11170. . 11233, 13292. . 13386)
/note="hypothetical protein"
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note-"Similar to Arabidopsis thaliana DNA chromosome

SAC clone F17A8; putative protein. (AL049482)"
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join(19096. 19172,20123. 20329,20389. 20395)
/note="hypothetical protein"
                                                                                                                        /cultivar="Nipponbare"
/db_xref="taxon:4530"
/db_xref="taxon:4530"
/chromosome="6"
/clone="p0029D06"
complement(join(1887. .2096,2316. .2390))
/note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TSGSAHEDEPDDEGGGGAGAEEEGGGSFSYKFKON"
join(8143. .8539,8557. .8908,9092. .9284)
/note="hypothetical protein"
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/note="hypothetical protein"
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/db_xref="GI:7363271"
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/db_xref="GI:7363273"
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/db_xref="G1:7363274"
                                                                                           /organism="Oryza sativa"
cocation/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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    FEATURES
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us-09-801-852a-3.rge

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79: gap of 100 bp 43521: contig of 2842 bp
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8344:
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                       COMMENT
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               44137. 44274,44361. 45333))
/note="ESTS C74776(ES1022),C26123(C116681) correspond to a region of the predicted gene.
Similar to Arabidopsis thaliana cultivar Landsberg extra-large G-protein (AF060942)"
                                                                                                                                                                                                                                              PVSYELPRIDPVDLPAIPTAQPVSGPLVPGRSNGVVADVVRPVFMPPVHRKQDAHRAE
PPPVAAQGRRRRSSESVDSAPQNEGFSDDDDSCSVSQESAHNFHGQRGGRTAAQEGRR
                                                                                                                                                                                                                                                                                               AQVVTFGVTEDSRYESKEFDDVSEQYVAVTKKEKRGRTCSRCGKRKWESKESCIVCDA
RFCSYCVLRAMGSMPEGRKCITCIGQPIDESKRSKLGKGSRILSRLLSPLESVRQILKA
                                                                                                                                                                                              /db_xref="G1:7363278"
/translation="MAGAGAVGGSNWEEMVRRMLPPGTTIPEAPANLDYSIALEYDGP
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 171574)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62981 CCTCGCCGCCGACGACTCCTCCCACCCTCCTCCTCCTCCCCGACTCCCCCCACTC 63040
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                                                                                                                                                                                                                                                                                                                                                                         3.1%; Score 68; DB 8; Length 150120;
1larity 53.4%; Pred. No. 0.1;
Conservative 0; Mismatches 125; Indels 0
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Homo sapiens chromosome 17 clone RP11-248L3 map 17,
IN PROGRESS ***, 48 unordered pieces.
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Homo sapiens chromosome 17, clone RP11-248L3
.42027,42111. .42288,42719.
                                                                                                                                          /codon_start=1
/protein_id="BAA93022.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1151 cgctgcggcgggcgtgaagaactcggcg 1178
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KEYWORDS
SOURCE
ORGANISM
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REFERENCE
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Research, 320 Charles Street, Cambridge, MA 02141, USA on MA 12, 2000 this sequence version replaced 91:6094565. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                          as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 48 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                       Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: Project Information
Center project name: L670
Center clone name: 248_L_3
                                                                                                                                                                                                                                                                                                                                                                                                               of 100 bp contig of 1235 bp in length of
                                                                                                                                                                                                                                                                                                                                                                                                                                                               contig of 1064 bp in length of 100 bp contig of 1139 bp in length of 1150 bp in length contig of 1150 bp in length
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f 1226 bp in length
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12118: contig of 1149 bp in

9 12218: gap of 100 bp

135141: contig of 1423 bp in

2 13741: gap of 100 bp

2 13584: contig of 1843 bp in
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contig of 1208 bp 1
ap of 100 bp:
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f 1079 bp f
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f 1039 bp
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22568: contig of 1138 bp
22668: gap of 100 bp
24914: contig of 2246 bp
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35389: contig of 2441 bp
35489: gap of 100 bp
37527: contig of 2038 bp
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contig of 2952 bp
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17014: contig of 1330 bp
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40579: cont
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18904: con
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20212: conf
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21330: con
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26711: con
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10770: cont
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35389: con
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4776: con
6: gap of
6026: con
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9543: con
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3537: con
3637: gap of
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10869: co
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1139 2373; co
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in length

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22 43621: gap of 100 bp 22 45931: contig of 2312 bp in length 34 46033: gap of 100 bp 24 48137: contig of 2704 bp in length 8 48837: gap of 100 bp 100 bp 10 55949: gap of 100 bp 100 bp
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147071 156784: contig of 9714 bp in length
156785 156884: gap of 100 bp
156885 171574: contig of 14690 bp in length.
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6469 bp in length
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124362: contig of 6111 bp in length
124462: gap of 100 bp
133078: contig of 8616 bp in length
                                                                                                                                                                                                                                                00 bp
3450 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                    63745: gap of 100 bp 66221: contig of 2476 bp in length 66321: gap of 100 bp 71307: contig of 4986 bp in length
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7475 bp in length
                                                                                                                                                                                                                                                                                                                                                                           60235: gap of 100 bp 63645: contig of 3410 bp in length
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103688: contig of 5476 bp in length
                                                                                                                                                                                                                                                                                                                                             contig of 4586 bp in length
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118151: contig of 6788 bp in length
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/clone_llb="RPCI-11 Human Male BAC"
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139647: contig of 6469 i
139747: gap of 100 by
146970: config of 7223
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note="assembly_fragment"
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139. 2373
note="assembly_fragment"
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note="assembly_fragment"
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10970. .12118
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12219. .13641
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Galactomyces geotrichum
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Galactomyces.
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2015. 26711
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2015. 30770
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Best Local Similarity 46.3%;
Matches 216; Conservative
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VERSION
KEYWORDS
SOURCE
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SINYRTGPYGFLGGDAITAEGNTNAGLHDQRKGLEWYSDNIANFGGDPDKVMIFGESA
GAMSVAHQLVAYGGDNTYNGKQLFHSAILQSGGPLPYFDSTSVGPESAYSRFAQYAGC
DASAGDNETLACLRSKSSDVLHSAQNSYDLKDLFGLLPQFLGFGPRPDGNIIPDAAYE
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YRGSWSEGAPFRIGILMALPPOFKRTAAIFPLLEQSPRKVMLNATKDVNRWYYLAT
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                                                                                                                             Direct Submission
Submitted (13-OCT-1993) Bertolini M., Biotechnology Research
Institute - NRCC, 6100 Royalmount Avenue, Montreal, Quebec H4P 2R2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation-"QAPTAVLNGNEVISGVLEGKVDTFKGIPFADPPVGDLRFKHPQF
                                   Polymorphism in the lipase genes of Geotrichum candidum strains
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Bertolini, M., Laramee, L., Thomas, D., Cygler, M., Schrag, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
9
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    1635
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                                                                                                                                                                                                                                                                                                                                                                                       /product="lipase"
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<1. .1635
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                                                                                                          Bertolini, M.
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JOURNAL
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AUTHORS
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Search completed: June 29, 2002, 15:19:58 Job time: 21479 sec

547 ACCAACGCTGGTCTGCACGACCAG 570

## GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

June 29, 2002, 09:21:59 ; Search time 7060.77 Seconds (without alignments) 5085.839 Million cell updates/sec Run on:

US-09-801-852A-1 1716 !itle:
Perfect score:

1 atgetecttaacetetteae......teteggtgaacgegggtete 1716 sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

1797656 segs, 10463268293 residues

Searched:

3595312 Potal number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:\* Database :

b\_om:\* b\_ov:\* b\_pat:

fun un q

em\_hum em\_in: em\_om:

em\_pat em\_or: em\_ov:

em\_sts

em\_htg\_hum:\*
em\_htg\_inv:\*
em\_htg\_other:\*

em\_htgo\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

A Query Match Length DB Score

SUMMARIES

502

AR034145 Sequence AX268013 Sequence BD005939 Cephalosp X66006 C.Cylindrac

102524 Geotrichum Sequence 5 G.cand1dum Geotrichum Geotrichum Geotrichum CDNA encod 102525 Geotrichum

Cephalosp

Rhodospo

CCLIPASE

AF044078

A81171 Sequence 1
X66007 C.cylindrac
A81172 Sequence 2
AF044078 Synthetic
X78032 G.geotrichu
AL357432 Streptomy
AL117385 Streptomy
AR233526 Drosophil
AR051959 Drosophil
AB070941 Streptomy

X74255 Sequence 11 X66008 C.cylindrac X64704 C.cylindrac X16712 C. cylindra

148377 Sequence 6 164703 C.cylindrac

E02497 cDNA encodi D00697 G.candidum AB000260 Geotrichu

J02623 Geotrichum J02625 Geotrichum

ALIGNMENTS

AB010632 Rattus no BC015290 Mus muscu AX121338 Sequence AP001046 Homo sapi

A45569 Sequence 7 A47607 Sequence 7 AR019333 Sequence AJ223965 Boophilus

Sequence 1 from Patent WO0166767. AX268011.1 GI:16516554 KEYWORDS SOURCE ORGANISM DEFINITION ACCESSION RESULT AX268011 VERSION

PAT 26-0CT-2001

linear

DNA

Rhodosporidium toruloides. Rhodosporidium toruloides Sukaryota, Fungi, Basidiomycota; Urediniomycetes; Microbotryomycetidae; Heterogastridiales; Sporidiobolaceae; Rhodosporidium. chiang, S.J. and Basch, J.D.
Chiang, S.J. and Basch, J.D.
Direct production of deacetyleephalosporin
Patent: WO 0166767-A 1 13-SEP-2001;
BRISTOL-MYERS SQUEB COMPANY (US) REFERENCE AUTHORS TITLE

1. .1716 /organism="Rhodosporidium toruloides" /db\_xref="taxon:5286" Location/Qualifiers

322

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sonrce BASE COUNT ORIGIN

JOURNAL

FEATURES

Description

Result Š

_	Oy 1021 actgagcgcgtcgctcc	1081	1141	1201	DD 1261 CCGTCAAAGGCCAACCT	1321	1381 TACGCGCGGCTCACAC		1501	1561	1621			ACCESSION AR034144 VERSION AR034144.1 GI:5 KRYWORDS SOURCE UNKNOWN	ORGANISM UNKNOWN. ORGANISM UNCLASSIfied. REFERENCE 1 (bases 1 to 1 ANTHONE POLITION.M. TON	TITLE Cephalosporin estation from the patent: US 58693 FATURES LOCATIO FEATURES 1.173	COUNT	Query Match 10 Best Local Similarity 10
	<pre>Query Match 100.0%; Score 1716; DB 6; Length 1716; Best Local Similarity 100.0%; Pred. No. 3.6e-235; Matches 1716; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</pre>	1 atgetecttaacetetteacectegeeteetegtgegaegeteeagetegeetttgee 60	61 tetecgacetecetegtecgecgcacgaacccaacgagececetecegtegtegacete 120	121 ggctacgccgctaccaaggctacttgaacgagaccgccggactctactggtggcgcgga 180 	181 atcgctacgcctcggctcagcgcttccaggctcctcagacgccgggacgcacaaggcc 240	241 gtccgcaacgcgactgagtatggaccgatctgttggccggctagcgagggaaccaacacg 300 	301 accaagggcttgccgccgcctagcaacagctcgagcagcgccgcagaaacaggcgtcg 360 . 	361 gaggattgcctcttcctcaatgtcgttgccccgccgccggtggagggcgacaatctt 420 	421 cccgtcttcgtctacattcacggaggtggctacgccttcggcgatgcgagcaccggcagc 480 	481 gactttgccgccttcaccaagcacacgggaaccaagatggtcgttgtaaatctccagtac 540 	541 cgtctcggcagctttggtttcctcgctggccaagccatgaaggactacggtgtaacgaac 600 	601 gccggcttgcttgaccagcaattcgccttcaatgggttcaacagcacgtctcgaagttc 660 	661 ggcggcaacccgatcacgttacgatttggggcgagtctgcagggcggggtcgttatg 720 	721 aaccagatcattgogaacggcggcaaccgtcaaggctctcggtctcaagaagccctc 780 	781 ttccacgctgccatcggctcctccgtcttcctcccaagccaagtacaactcccc 840	841 ttcgccgagctgctctactcccaactcgtctcggcgacaaactgcaccaaagccgcctcg 900 	901 tccttcgcttgcctcgaagctgtcgacgctgcggcgctcgct	961 tcggoggcgttcccgttcgggttttggtcgtatgtcccggtcgtcgacgggaccttcttg 1020 
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                     Score 1716; DB 6; Length 1738; Pred. No. 3.6e-235;
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patent US 5869309.
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1738 bp DNA linear PAT 31-JAN-2002 orin esterase gene from Rhodosporidium toruloides. SP-1997 JP 1998514766 SP-1996 US 60/026929 NEL POLITINO, SEAN M TONZI, JOHN J USHER, WILLIAM V BURNETT, ROMANOIK 1 to 1738)

1, Tonzi,S.M., Usher,J.J., Burnett,W.V. and Romanc,G.

20101501466.A 1 06-FEB-2001;

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FEATURES source	Location/Qualifiers 11738 /organism="unidentifi	Db 911 TCTTCGCTTGCCTCGAAGC	1111 AAGC
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Query Best L	Query Match 100.0%; Score 1716; DB 6; Length 1738; Best Local Similarity 100.0%; Pred. No. 3.6e-235; Matches 1716; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1021	tccti 
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Oy 841 Db 851	41 ttcgccgagctgctctactcccaactcgtctcggcgacaaactgcaccaaagccgcctcg 900 	REFERENCE 1 (bases 1 to RUTHORS POLITIO,M., TC	n. 173 Tonzi
Qy 901	1 tecttegettgeetegaagetgtegaegetgeggegetegetgegggegg		and c n tor

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Submitted (15-SEP-1997) Biotechnology Bristol-Myers Squibb Co., 6000 Thompso 13057-5050, USA
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1. 1738
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Gaps 9

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Cephalosporin esterase gene from Rhodosporidium toruloides.
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S POLITINO,M., Tonzi,S.M., Usher,J.J., Burnett,W.V. and Romanc,G Cephalosporin esterase gene from Rhodosporidium toruloides
C PREDICT OF SOUTSOURCE,A 2 06-FEB-2001;
BRISTOL MYERS SQUIBB CO
S Unidentified
PN JP 2001501466-A/2
PP 11-SEP-1997 JP 1998514766
PR 18-SEP-1997 JP 1998514766
PR 18-SEP-1996 S 60/026929
PI MICHAEL POLITINO,SEAN M TONZI,JOHN J USHER,WILLIAM V BURNI GUNA ROMANCIR
PC C12P21/06,C12N1/00,C12N9/16,C12N15/00
CC Strandedness: Double;
CC Topology: Linear;
FH Key Linear;
FT source /organism='Unidentified'.
                                                                                                                                                                                           GCCACTATTCAGAACGACACGATCAGCGACCAGTCGCAGCGCGTCTCCCAGTTCGACCGC
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JP 2001501466-A/2.
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SOURCE
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AUTHORS
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6 qq	Oy 8	Oy 8	6y 9 Db 11	Oy 10			DD 133	Db 13	Oy 112: Db 1457	Oy 11	Oy 12 Db 15	Oy . 13	0y 13	Qy 13 Db 17	Qy 14	Oy 14	Oy 15 Db 15	Oy 16	OY 166 Db 205

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MAAYPQDITQGLPFDTGIFNAITPQFKRILAVLGDLAFIHARRYFLNHFGGGTKYSFL
LKQLLGLPIMGTFHANDIVWQDYLLGSGSVIYNNAFIAFATDLDPNTAGLLVNWPKYT
SSLQLGNNLMMINALGLYTGKDNFRTAGYDALMTNPLLFFV"
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EPPYGNLRFKDPVPYSGSLNGQKFTLYGPLCMQONPEGTFEENLGKTALDLVMQSKVF
PLN 30-JUN-1993
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See X66006-8, X16712, X64703 & X64704
X66006, X66007 and X66008 are related sequences in the description
of C.cylindracea Lip1 and Lip2 sequences (X64703, X64704).
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GKPIIHVAVNYRVASWGFLAGDDIKAEGSGNAGLKDQRLGMQWYADNIAGFGGDPSKV
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FVSSAGCGSASDKLACLRSALSDTLLDATNNTPGFLAYSSLRLLYLPRPDGKNITDDM
                                                                                                                                                                               Eukaryota; Fung1; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; mitosporic Saccharomycetales; Candida.
1 (bases 1 to 1855)
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                                                                                                                                                                                                                                              Longhi, S.

Longhi, S.

Direct Submission
Submitted (06-MX-1992) S. Longhi, Universita' degli Studi di
Milano, Via Celoria 26, 20133 Milano, ITALY
(bases i to 1855)
Lotti, M., Grandori, R., Fusetti, F., Longhi, S., Brocca, S.,
Tramontano, A. and Alberghina, L.
Cloning and analysis of Candida cylindracea lipase sequences
Gene 124 (1), 45-55 (1993)
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219. .1730
/gene="LIP3"
/EC_number="3.1.1.3"
/product="triacylglycerol lipase"
a 595 c 523 g 376 t
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/protein_id="CAA46805.1"
/db_xref="GI:1325989"
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/strain="ATCC 14830"
       DNA
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/clone_lib="SACI genomic"
84. .218
'qene="LIP3"
84. .1733
     1855 bp
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/codon_start-1
                       C.cylindracea LIP3 gene.
X66006 S55937
X66006.1 GI:296933
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Galactomyces geotrichum

Eukaryota; Fung1; Ascomycota; Saccharomycotina; Saccharomycetales; Dipodascaceae; Galactomyces.

1 (bases 1 to 1635)

Alibert,G., Mouloungui,Z. and Boudet,A.

METHOD FOR PRODUCING FATTY ACIDS OR DERIVATIVES THEREOF
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Pred. No. 2.9e-06;
0; Mismatches 170; Indels
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/db_xref="taxon:27317"
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Other publication AN 29849595 960222
Other publication FR 2722798 960126
Location/Qualifiers
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Sequence 5 from Patent WO9603511.
A48376
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sal Similarity 56.1%;
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DASAGDNETLACLRSKSSDVLHSAQNSYDLKDLFGLLPQFLGFGPRPDGNIIPDAAYE
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OLHNLVPFLGTFHGSDLLFQSYVDLGPSSAYRRYFISFANHHDPNVGTNLKOWDMYTD
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EDCLYINVFRPAGTKPDAKLPVMVWIYGGAFVFGSSASYPGNGYVKESVEMGQPVVFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (13-OCT-1993) Bertolini M., Biotechnology Research
Institute - NRCC, 6100 Royalmount Avenue, Montreal, Quebec H4P 2R2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polymorphism in the lipase genes of Geotrichum candidum strains Unpublished
                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (sites)
Bertolin1,M., Laramee,L., Thomas,D., Cygler,M., Schrag,J. and
                                                                                             cagtaccgtctcggcagctttggtttcctcgctggccaagccatgaaggactacggtgta
CCGGTCATGCTCTGGATCTTTGGCGGTGGGTTTGAGATCGGCAGCCCCACCATCTTCCCT
                                 gactttgccgccttcaccaa----gcacacgggaaccaagatggtcgttgtaaatctc
                                                           CCCGCCCAGATGGTCACCAAGAGTGTGTCATGGGCAAGCCCATCATCCACGTGGCCGTC
                                                                                                                                                               acgaacgccggcttgcttgaccagcaattcgcccttcaatgggttcaacagcacgtctcg
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Geotrichum candidum NRRL Y-552 lipase gene, partial י
U02524
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Eukaryota; Fungi; Ascomycota; Saccharomycotina;
Saccharomycetales; Dipodascaceae; Galactomyces.
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Pred. No. 1.9e-06;
0; Mismatches 166;
                                                                                                                                                                                                                                                                                        /product="lipase"
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Bertolini, M.
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Best Local Similarity 56.6
Matches 224; Conservative
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SINYRTGPYGFLGGDATAEGNTNAGLHDORGGLEWYSDNIANFGGDPDKVMIFGESA
GAMSVAHQLVAYGGDNIYNGKKLFHSALLQSGGPLPYFDSTSVGPESAYSRFAQYAGC
DASASDNETLACLRSKSSDVLHSAQNSYDLKDLFGLLPQFLGFQRPRDGNIIPDAAYE
LYRSGRYAKVPYITGNDEDGTILAPVAINATTPHVKKWLKYICSEASDASLDRYLS
LYRGSRASAPFRTGILNALTPQFKRIAAIFTDLLFQSPRRYMLNAFKDVNRYTLAY
QLHNLYPFLGTFHGSDLLFQYYVDLGPSSAYRRYFISFANHHDPNVGTNLKQWDMYTD
AGKEMLQIHWVGNSMRTDDFRIEGISNFESDVTLFG"
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EDCLYLNVFRPAGTKPDAKLPVWWIYGGAFVFGSSASYPGNGYVKESVEMGQPVVFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (05-OCT-1993) Bertolini M., Biotechnology Research
Institute - NRCC, 6100 Royalmount Avenue, Montreal, Quebec H4P 2R2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polymorphism in the lipase genes of Geotrichum candidum strains
                                                                                                                                                                                                                                                                                                                         CCCGTCATGGTTTGGATCTACGGTGCTGCCTTTGTGTTTGGTTCTTCTGCTTCTTACCCT 426
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 cccgtcctcctacattcacggaggtggctacgccttcggc----gatgcgagcacc 474
                                                                         ggcagcgactttgccgccttcaccaagcacacgggaaccaagatggtcgttgtaaatctc 534
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    1635
/organism="Galactomyces

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Bertolini, M.
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GAMSVAHQLIAYGGDNTYNGKQLFHSAILQSGGPLPYFDSTSVGPESAYSRFAQYAGC
DTSVSDNDTLACLRSKSSDVLHSAQNSYDLKDLFGLLPQFLGFGFPFDGNIIPDAAYD
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/translation="QAPTAVINGNEVISGVLEGKVDTFKGIPFADPPVGDLRFKHPQP
FTGSYQGLKANDFSSACMQLDPGNAISLLDKVVGLGNILPDNLRGPLYDMAQGTVSMS
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LYRGSWSEGAPFRIGILMALPPOPKRIAAIFPDLLEOSPRKVMLNATKOVNRWYYLAT
QLHNLVPFLGTFHGSDLLFQYVVDLGPSSAYRRYFISFANHHDPNVGTNLOOWDMYTD
AGKEMLOIHMIGNSMTDDFRIEGISNPESDVTLFG
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Box 339,
                                                                                                                                                                                                                                                                                                                                                                                                                              Galactomyces geotrichum.
Galactomyces geotrichum.
Galactomyces geotrichum.
Eukaryota; Fungi; Ascomycota; Saccharomycetles;
Saccharomycetales; Dipodascaceae; Galactomyces.

1 (bases 1 to 1635)
Pretorius, G. H.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (16-SEP-1994) G.H.J. Pretorius, University of the Oral
Free States, Dept of Microbiology and Biochemistry, PO Box 339,
Bloemfontein, 9300, SOUTH AFRICA
2 (bases 1 to 165)
Phillips, A., Pretorius, G.H. and van Rensburg, H.G.
Molecular characterization of a Galactomyces geotrichum lipase,
another member of the cholinesterase/lipase family
Blochim. Blophys. Acta 1252 (2), 305-311 (1995)
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acgaacgccggcttgcttgaccagcaattcgcccttcaatgggttcaacagcacgtctcg
                                                                                           ACCAACGCTGGTCTGCACGACCAGCGCAAGGGTCTCGAGTGGGGTTAGCGACAACATTGCC
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/organism="Galactomyces geotrichum"
/strain="CBS 178 71"
/db_xref="taxon:27317"
                                                                                                                                                                                                          gttatgaaccagatcattgogaacggcaacaccgtcaa 755
                                                                                                                                                                                                                                  667 GTTGCTCACCAGCTTGTTGCTACGGTGGTGACAACACTA 707
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/protein_id="CAA57316.1"
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Pred. No. 2.9e-06;
0; Mismatches 170;
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Best Local Similarity 56.1%;
Matches 225; Conservative
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Schrag, J.

Length 1635; Score 107; DB 8; Pred. No. 2.9e-06; 6.2%; 56.1%; Query Match Best Local Similarity ï

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GCU02622 1635 bp DNA linear PLN 22-OCT-1993
Georgichum candidum ATCC 34614 lipase gene, partial cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (21-OCT-1993) Bertolini M., Biotechnology Research
Institute-NRCC, 6100 Royalmount Avenue, Montreal, Quebec, H4P 2R2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomycetes;
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Bertolin1,M., Laramee,L., Thomas,D., Cygler,M., Schrag,J. and
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9
                                                                                     Length 1635;
                                                                                   Score 107; DB 8; Length 16
Pred. No. 2.9e-06;
0; Mismatches 170; Indels
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    /organism="Galactomyces

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                                                                                   Query Match 6.2%;
Best Local Similarity 56.1%;
Matches 225; Conservative
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Bertolini, M.
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IPYOTLSVGSBFRTGILNATTPGKRYAAILSDMLFQGRRYALSATKOVNRWYYLST
HLHNLVPFLGTFHGNELI RQFNVNIGPANSYLLSY FISFANHHDPNVGTNLLQWDQYTD
EGKEMLEIHWTDNYRTDDYRIEGISNFETDVNLYG"
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FTGSYQGLKANDFSPACMQLDPGNSLTLLDKALGLAKVIPEEFRGPLYDMAKGTVSMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (14-OCT-1993) Bertolini M., Biotechnology Research
Institute - NRCC, 6100 Royalmount Avenue, Montreal, Quebec H4P 2R2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SINYRTGPFGFLGGDAITAEGNTNAGLHDQRKGLEWVSDNIANFGGDPDKVMIFGESA
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Eukaryota, Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Dipodascaceae; Galactomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polymorphism in the lipase genes of Geotrichum candidum strains
                                           gaggattgcctcttcctcaatgtcgttgcccccgccggctcgtgcgagggcgacaatctt 420
                                                               cccgtcctcgtctacattcacggaggtggctacgccttcggc----gatgcgagcacc 474
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    Gaps
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Bertolini,M., Laramee,L., Thomas,D., Cygler,M.,
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/organism="Galactomyces geotrichum"
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  170;
  Mismatches
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/protein_id="AAA03430.1"
/db_xref="GI:408469"
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/db_xref="taxon:27317"
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Bertolini, M.
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  Conservative
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Matches 223; Conserva
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PF 27-MAR-1989 JP 1989074721

PI SHIMDA VUJI, TOMINACA YOSHIO, SUGIHARA AKIO, IIIZUMI TARO PC C12N15/55/C12N9/20, (C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/55/C12N15/5
GAMSVAHQLVAYGGDNTYNGKQLFHSAILQSGGPLPYFDSTSYGPESAYSRFAQYAGC
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QLHNIVPFLGTFHGSDLFLOYYVDLGPSSAYRRYFISFANHHDPNVGTNLKQMDMYTD
SGKEMLQIHMIGNSMRTDDFRIEGISNFESDVTLFG"
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Galactomyces geotrichum.

Galactomyces geotrichum.

Galactomyces geotrichum.

Backaryota; Fungil, Ascomycota; Saccharomycotina; Saccharomycetes;

Sackaromycetales; Dipodascacee; Galactomyces.

I (bases 1 to 1692)

Shimada,Y., Tominaga,Y., Sugihara,A. and Ilizumi,T.

GENE OF PROTEIN HAVING LIPASE ACTIVITY

PATER IND LTD, OSAKA CITY

N WATER IND LTD, OSAKA CITY

OS Geotrichum candidum

PN 199029588-A/1

PD 11-DEC-1990
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Pred. No. 3.1e-06;
0; Mismatches 167; Indels
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CDNA encoding lipase.
E02678
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JP 1990299588-A/1.
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Best Local Similarity 56.3
Matches 223; Conservative
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                                                                                      1. .1692
/organism-"Galactomyces geotrichum"
//db_xref="taxon:27317"
/ 466 c 403 g 487 t
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Pred. No. 3.1e-06;
0; Mismatches 167
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                                   1, .1692
/product-'llpase'
Location/Qualifiers
                    /product='lipase'
1. .1692
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llarity 56.3%;
Conservative 0
   58.
mat_peptide
FT CDS
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Mon Jul 1 14:07:44 2002

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620 bp mRNA linear EST 01-MAY-2001 D00142-R Lambda Zap, Stratagene Blumeria graminis f. sp. hordei CDNA clone D00142 similar to lipase 2 precursor, mRNA sequence. AN790714 EST. EST. EST. EST.
                                                                                     ALO75102 Drosophil
B133222 60298365
B1626691 RH67704.5
Be636568 rockefell
AL527918 uj30g104.y
AA230461 my30811.r
AU003170 AU003170
Be636721 rockefell
AA377049 EST89551
BN37703 EST89551
BR374709 EST89551
                                                                                                                                                                                                             AI108156 GH06911.5
AI108080 GH06811.5
BI31296 602982970
BI146926 60291853
BI220765 602938883
BI33230 60299593
AI1062034 GH01076.5
A1527908 uj30f03.y
B1574042 RH09457.5
AA246278 LD05065.5
BR256789 HVSMEf001
BC263795 WHE2338_B
BG970699 602838590
BG969645 6028365983
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blumeria graminis f. sp. hordei.
Blumeria graminis f. sp. hordei
Bukaryota; Fundi, Ascomycota; Pezizomycotina; Leotiomycetes;
Erysiphales; Erysiphaceae; Blumeria.
1 (bases 1 to 620)
Thomas, S.W., Rasmussen, S.W., Glaring, M.A., Rouster, J.A. and Oliver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 y R.P. Gene identification in the fungal pathogen Blumeria graminis by Gene identification in the fungal pathogen Blumeria graminis by myprassed sequence tag analysis Unpblished (2000)
Contact: Rasmussen, S.W.
Contact: Rasmussen, S.W.
Carlsberg Laboratory
Carlsberg Laboratory
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1. .620
//organ="Blumeria graminis f. sp. hordei"
/db xref="taxon:62688"
/clone="D00142"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 Gl. Carlsbergvej, DK-2500, Copenhagen, Denmark
Tel: 45 3327 5230
Fax: 45 3327 4766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Lambda Zap, Stratagene"
/cell_type="conidia"
/lab_host="Hordeum vulgare"
165 c 147 g 160 t
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                                 BF256789
BG263795
BG263795
BG36845
A1516721
CNS01029
B1332322
B1626691
BE63658
A1527918
AA230461
AU03170
BE636721
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    ORIGIN
                                                                            June 29, 2002, 09:17:09; Search time 4149.72 Seconds (without alignments) 5581.286 Million cell updates/sec
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AA415091 MG0026 RC
BE721206 602999553
AA202160 LD02242.5
BF385648 602047302
BF785601 602112390
AL150081 Anopheles
B1460262 603201884
B1554561 603235901
BC015286 Mus muscu
AF508950 vc28803.y
BE490305 WHE03592
B1564560 RHE03592
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W512144 xu54e11.x
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1716
1 atgctccttaacctcttcac......tctcggtgaacgcgggtcic 1716
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             GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                      13736207 seqs, 6748477542 residues
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Maximum Match 100%
Listing first 45 summaries
                                                         - nucleic search, using sw model
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BF785601
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60393953F1 NCI_CGAP_L19 Mus musculus cDNA clone IMAGE:5102701 5',
B1221206
E1221206.1 GI:14674650
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 727)
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/clone="IMAGE:5102701"
/clone="Lib="NGI_CGAP_Lig="
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/note="Organ: liver; Vector: pCMV-SPORT6; Site_l: Not1;
Site_2: Sali; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

191 c 200 g 184 t
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Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1247 row: j column: 14
High quality sequence start: 6
High quality sequence store: 692.
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National Institutes of Health, Mammalian Gene Collection (MGC)
taccgtctcggcagctttggtttcctcgctggccaagccatgaaggactacggtgtaacg
                                                                418 cttcccgtcctcgtctacattcacggaggtggctacgccttcggcgatgcgagcaccggc
                                                                                                                                                478 agcgactttgccgccttcaccaagcacacgggaaccaagatggtcgttgtaaatctccag
                                                                                                                                                                                        522 TACGACGGCACAGGGCTGGTCAAGGCCGGCGATTACGGCCTGATCGCCATAACTTTCAAC
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/organism="Mus musculus"
/strain="FVB/N"
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//dev_stage="Day 5 post-inculation"
//note="Vector: Lambda Zap; Messenger RNAs prepared from Magnaporthe grisea grown at 23C in the dark with constant gyracory shaking (100 rpm) in Vogel's medium containing of 1s isolated cell walls as the sole carbon source"
542 c 533 g 345 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA415091 1800 bp mRNA linear EST 09-DEC-1999 Mg0026 RCW Lambda Zap Express Library Magnaporthe grisea CDNA clone RCW26 similar to Triacylglycerol Lipase (EC 3.1.1.3), mRNA
                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wu,S.-C., Bernstein,B.D., Darvill,A.G. and Albersheim,P. Expressed sequence tags of the rice blast fungus grown on rice cell
                                                                                                                                                                                                                                  tegecetteaatgggtteaacageacgtetegaagtteggeggeaacecegateacgtta 682
                                                                                                                                                                                                                                                                                                                      742
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                                                                                                                                                                                                                                                                                                                                              212 CICITITICGGRACITCTGCAGGIGGIAICICCACATGGAACCIGITGACIGCCAAGGACG 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe. (bases 1 to 1800)
                                                                503 acacgggaaccaagatggtcgttgtaaatctccagtaccgtctcggcagctttggtttcc 562
                                                                                                                                                tegetggecaagecatgaaggactacggtgtaacgaacgccggettgettgaccagcaat 622
                                                                                                                                                                            TECTICIACAATGGGTTCAAGATAACATCGCCAAATTCGGTGGTGATCCAGAAAAGGTTA
                                                                                                        32 ACAACGGAAGCCAATTGTCTACATTGCCGTCAACTACCGTCTTGGTGCCTTTGGATGGT
                                                                                                                                                                                                                                                                                                                        cgatttgggggggggtctgcaggcgcagggtccgttatgaaccagatcattgcgaacggcg
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52.5%; Pred. No. 0.039;
iive 0; Mismatches 175; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="RCW26"
/clone_lib="RCW Lambda_Zap Express Library"
                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             University of Georgia
220 Riverbend Road, Athens, GA 30602-4712,
Tel: 706 542 4446
Fax: 706 542 4412
Email: wuscebscr.uga.edu
Fully sequenced
  Pred. No. 0.00073;
0; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Magnaporthe grisea"
/strain="CP987"
/db_xref="taxon:148305"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Std Error: 0.00.
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1. .1800
                      ó;
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58.0%;
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Magnaporthe grisea
                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              207; Conservative
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    Best Local Similarity
Matches 142; Conserv
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BF385648 810 bp mRNA linear EST 27-NOV-2000 602047302F1 NCI_CGAP_L19 Mus musculus cDNA clone IMAGE:4196665 5',
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 810)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="FVB_N"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone_lib="NCL_CGAP_Li9"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: liver; Vector: pCMY-SPORT6; Site_1: NotI;
/note="Cran: cloned unidirectionally. Primer: Oligo dT. Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   305 TCCGAGGACTGCCTTTTCCTTAATGTATGCACCTAAAGTCAAAAGTACGCGGACTCCT 364
                                                                                                                                                                                            365 TTACCCGTGATGGTCTGGATTCATGGTGGAGGCTTCTTCTTCGGCAACGGCAACAGTGAC 424
                                                                                                                                                                                                                                                                                                            425 Trccactrrcccg-----ccaaccrcargaagcaggaggacarrcrgacccrgaar 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                        aacgccggcttgcttgaccagcaattcgcccttcaatgggttcaacagcacgtctcgaag 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9534 row: c column: 02
High quality sequence stop: 700.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                           479 TACCGACTTGGAGCGCTTGGTTTCCTTAGTCTGCCCGAGGAGGAATACACGG-----C
                                                                                                                                                                      cttcccgtcctcgtctacattcacggaggtggctacgccttcggcgatgcgagcaccggc
                                                                                                                                                                                                                                                                                                                                                                 taccetctcggcagctttggtttcctcgctggccaagccatgaaggactacggtgtaacg
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Email: cgapbs r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                  agogactttgccgccttcaccaagcacacgggaaccaagatggtcgttgtaaatctccag
  Pred. No. 0.078;
0; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tteggeggeaacecegateacgttacgattt 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              593 TTCAATGGCGATCCGAATAACGTAACGCTCT 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
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  Local Similarity 55.0%;
es 182; Conservative
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AUTHORS
TITLE
JOURNAL
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                        5
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/clone_lb-"LD Drosophila melanogaster embryo BlueScript"
/sex="male and female"
/dev_stage="0" to 24 hours mixed stage embryonic"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA202160
LD02542.5prime LD Drosophila melanogaster embryo BlueScript
Drosophila melanogaster cDNA clone LD02542 5prime, mRNA sequence.
                                                                                                                                                                                                 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      351 acaggcgtcggaggattgcctcttcctcaatgtcgttgcccccgccggctcgtgcgaggg 410
                                                                                                   411 cgacaatcttcccgtcctcgtctacattcacggaggtggctacgccttcggcgatgcgag 470
                                                                                                                                                                                                                                                                  caccggcagcgactttgccgccttcaccaagcacacgggaaccaagatggtcgttgtaaa 530
                                                                                                                                                                                                                                                                                                               ----TGGTGGTGGTGAC 491
                                                                                                                                                                                                                                                                                                                                                                                                           492 CATTCAGTATCGCCTTGGCATCTGGGGATTCTTCAGC----AACTGGGGATGAACACAG 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 25 row: D column: 6
High quality sequence stop: 484.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                              531 tctccagtaccgtctcggcagctttggtttcctcgctggccaagccatgaaggactacgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  607 TGCCAACTTGGGGGGCAACCCAGGCTCGGTGACCATCTTTGGAGTCAGCAGGAG 662
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                        Indels
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/db_xref="BDGP_EST:BDc1n002213"
/db_xref="taxon:7227"
Pred. No. 0.074;
0; Mismatches 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                               441 CACCTATGATGGACTGGCCCTCTCTGCCCATGAAATG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster
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Contact: Stapleton, M.
ilarity 53.9%;
Conservative
  Similarity
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  Local Sim
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  Best Loc
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AUTHORS
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AA202160
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Length 810;
Score 67.2; DB 10;
Pred. No. 0.1;
3.98;
Query Match
Best Local Similarity
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Length 625;

6 DB

Score 67.8;

4.0%;

Query Match

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CNSOLLTS
Anopheles gambiae GSS SP6 end of clone 20C0l of NotreDamel library from strain PEST of Anopheles gambiae (African malaria mosquito),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                         gaggattgoctetteeteaatgtegttgeeeegeeggetegtgegagggegaeaatett 420
                      357 gtcggaggattgcctcttcctcaatgtcgttgcccccgccggctcgtgcgagggcgacaa 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr. Roux, Paris 75015, France
This clone is from an A. gambies BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roth, C.W., Brey, P.T., Ke, Z., Collins, F.H. and Weissenbach, J. 
Direct Submission
                                                                                                                                                                                                                                         506 TGATGGATCTCTATTGACAGTCAATGA-----GGACTTGGTGGTTGTTACTATCCA
                                                                                                                                                                                                                                                                                    gtaccgtctcggcagctttggtttcctcgctggccaagccatgaaggactacggtgtaac
                                                                GTCTGAGGACTGCCTGTATCTCAACATCTACACCCCAGCCCCATGCCCATGAGGGCTCTAA
                                                                                                             tettecegtectegtetacatteacggaggtggetacgeetteggegatgegageacegg
                                                                                                                                    cagcgactttgccgccttcaccaagcacacgggaaccaagatggtcgttgtaaatctcca
                                                                                                                                                                                                                                                                                                                           557 GTATCGTCTGGGTGTCCTGGGCTTTTTCAGCACTGGAGACCAGCATGCCAGAGG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 783;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
Pteryyota; Neoptera; Endopterygota; Diptera; Nematoce
(Culicoidea; Anopheles
1 (bases 1 to 783)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gttcggcggcaaccccgatcacgttacgatttggggcgagtctgcaggcg 706
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/organism="Anopheles gambiae"
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/clone="20001"
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(bases 1 to 783)
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BF785601
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/clone="ID="NCI_CGAP_Kid14"
/lab_host="DHIDB (TI phage-resistant)"
/note="Organ: Kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"
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Subaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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  0; Mismatches 148;
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High quality sequence stop: 757.
Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninot (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Plate: LLAM11675 row: g column: 22
High quality sequence stop: 525.
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Contact: Robert Strausberg, Ph.D.
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/clone_lib-"NCI_CGAP_SG2"
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/lab_host-"DH10B (Tl_phage-resistant)"
/note-"Organ: salivary gland; Vector: pCMV-SPORT6; Site_l:
Not1; Site_2: Sall; Cloned unidirectionally. Primer: Oligo
dT. Average insert size 1.3 kb. Constructed by Life
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NIH-MGC http://mgc.nc1.nlh.gov/.
National institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     googgettgettgaccageaattegeeetteaatgggtteaacageacgtetegaagtte 660
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                                                                                                                     361 gaggattgcctcttcctcaatgtcgttgcccccgccggctcgtgcgagggcgacaatctt 420
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Tissue procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life T.M.A.G.E. Consortium
(LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can lette://image.llnl.gov
http://image.llnl.gov
plate: LLAMI0815 row: a column: 16
High quality sequence stop: 724.
                                                                                                                                                                                                                                                                                                                                                       gactttgccgccttcaccaagcacacgggaaccaagatggtcgttgtaaatctccagtac
                                                         15;
Score 65; DB 10; Length 526
Pred. No. 0.22;
0; Mismatches 160; Indels
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/db_xref="taxon:10090"
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      3.8%;
   Ouery Match 3.8
Best Local Similarity 52.8
Matches 196; Conservative
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BG867060
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5;

15;

DB 10; Length 973;

ų 260 530

514

590 568 650 628

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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 1942)
Strausberg,R.
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CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Array Preparation: Life Technologies, Inc.

CDNA Library Array Preparation: Life Technologies, Inc.

DNA Sequencing Dy: Sequencing Group at the Stanford Human Genome

Center, Stanford University School of Medicline, Stanford, CA 9430

Contact: (Dickson, Mark) mcdepaxil.stanford.edu

Contact: (Dickson, Mark) mcdepaxil.stanford.edu

Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (01-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 25 Row: 1 Column: 4
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein This clone has the following problem: frame shifted.

Location/Qualifiers
                                                                                                                                                                                                351 acaggogicgogaggattgcctcttcctcaatgicgitgcccccgccggctggtgggggg 410
                                                                                                                                                                                                                                                                                               411 cgacaatcttcccgtcctcgtctacattcacggaggtggctacgccttcggcgatgcgag 470
                                                                                                                                                                                                                                              344 ACAGITITICIGAAGACIGCCICIACCIGAAIAITIACACICCIGCIGACIIGACAAAGAA 403
                                                                                                                                                                                                                                                                                                                                caccggcagcgactttgccgccttcaccaagcacacgggaaccaagatggtcgttgtaaa
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                                                                                                 Score 64; DB 10; Length 97.
Pred. No. 0.35;
0; Mismatches 150; Indels
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
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BC015286.1 GI:15929725
                                                                                                   3.78;
                                                                                                   Query Match
Best Local Similarity 53.4
Matches 189; Conservative
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AUTHORS
TITLE
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 973)
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/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: liver; Vector: pCWY-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                            acaggogtoggaggattgootottcotcaatgtogttgoocoogooggotogtgogaggg 410
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Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Sequencing by: Thorte Genomics, Inc.
Clone distribution: MGC clone distribution information can if cound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1785 row: b column: 01
High quality sequence stop: 702.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         651 ctcgaagttcggcggcaaccccgatcacgttacgatttgggggcgagtctgcaggcg 706
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Technologies. Note: this is a NCI_CGAP Library." 178 c 189 g 196 t
                                                                                                                                                                           15;
                                                                                                                             Length 725;
                                                                                                                                                                           Indels
                                                                                                                        Score 64.4; DB 10;
Pred. No. 0.29;
0; Mismatches 151;
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/clone="IMAGE:5309856"
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BI554561.1 GI:15441875
                                                                                                                        3.8%;
ilarity 53.4%;
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Vo28803.91 Barstead MPLRB1 Mus musculus cDNA clone IMAGE:775852 5'
similar to gb:L07765 LIVEA MASSULESTERASE PRECURSOR (HUMAN);
gb:M57960 Mouse carboxylesterase mRNA, complete cds (MOUSE);, mRNA
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (2008) 1 (455)

Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,

Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, F., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Pape, D., Harvey, N., Schurk, R., Ritter, Waterston, R. and Wilson, R.

The Washu-NCI Mouse EST Project 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     read is a RESEQUENCE of a previously sequenced mouse clone
                                                                                                                       month old male mouse."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      356 cgtcggaggattgcctcttcctcaatgtcgttgcccccgccggctcgtgcgagggcgaca 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     416 atcttcccgtcctcgtctacattcacggaggtggctacgccttcggcgatgcgagcaccg 475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        476 gcagcgactttgccgccttcaccaagcacacgggaaccaagatggtcgttgtaaatctcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      agtaccgtctcggcagctttggtttcctcgctggccaagccatgaaggactacggtgtaa
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Fax: 314 286 1810
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Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:4239608"
/tissue_type="Kidney, normal, 5 mo.
/clone_lib="NCI_CGAP_Kid14"
/lab_host="DH108"
/note="Vector: pCWY-SPORT6"
a 494 c 487 g 490 t
                                                                                                                                                                                                                                                                                                                                                                                                 3.6%; Score ... 0.65; 53.3%; Pred. No. 0.65; ... 0; Mismatches 149; ... 0; Mismatches 149; ... 0; Mismatches 149; ... 0; Mismatches 149; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0; ... 0
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AIS08950.1 GI:4407855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 187; Conservative
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AIS08950
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
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VERSION
KEYWORDS
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JOURNAL
COMMENT
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BE490305 EST 31-JUL-2000 WHE0359_B09_C172S Wheat cold-stressed seedling cDNA library Triticum aestivum cDNA clone WHE0359_B09_C17, mRNA sequence. BE490305
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3/]; double-stranded cDNA was ligated to Eco RI adaptors [CATCGGATTCGGTACC], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead."
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This read has been verified (found to hit its original self in the correct orientation)
Seq primer: -4.0RP from Glbco
High quality sequence stop: 421.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker, Sife_1: EcoRis Site_2: Noti; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' regrated cont is the a Not I - oligo(dT) primer [5' regrated cont is the a Not I - oligo(dT) primer [5' regrated cont is the a Not I - oligo(dT) primer [5' regrated cont is the all the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Han
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     351 acaggogtoggaggattgcotottcotcaatgtogttgcoccogcoggotogtgcgaggg 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            471 caccggcagcgactttgccgccttcaccaagcacacgggaaccaagatggtcgttgtaaa 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       531 tetecagtacegteteggeagetttggttteetegetggeeaageeatgaaggaetaegg 590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260 regeggaaacregegreacrregaceaegregerecacregeregerecaggacaacar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tgtaacgaacgccggcttgcttgaccagcaattcgcccttcaatgggttcaacagcacgt
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Pred. No. 0.66;
0; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 others
                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Barstead MPLRB1" /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 t
                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/strain="BALB/c"
                                                                                                                                                                                                                                                                                                                                                                    /db_xref-"taxon:10090"
/clone="IMAGE:775852"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Kidney"
/dev_stage="6 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Triticeae; Triticum.
1 (bases 1 to 564)
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Best Local Similarity 52.5%;
Matches 187; Conservative (
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AUTHORS
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Mon

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Drosophila melanogaster cDNA clone RH61852 5 similar to clt:
FBan0009858 GO:[carboxyesterase (GO:0004091); carboxyesterase
(GO:0004091)] located on: 2R 57F4-57F4;; 08/23/2001, mRNA sequence.
                                                                                                                                                             Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Eukaryota; Metazoa; Arthropoda; Tracheata; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (Dases 1 to 676)

Stapleton,M., Brokstein,P., Hong,L., Tyler,D., Berman,B., Carlson,R., Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E., George,R., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G., Misra,S.,

Mungall,C.J., Nunoo,J., Pacleb,J., Paragas,V., Park,S.,

Phouanenavong,S., Wan,K., Yu,C., Lewis,S.E., Celniker,S. and Rubin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-Torgan: head; Vector: pFlc1; Site_1: Xho1; Site_2: BamHI: Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="RH Drosophila melanogaster normalized Head
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             494 Trccacrificce-----ccaagcrcargaagcagaagaagrcarrargaccaccrgaar 547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003454: arm:2R [16312727,16613591]
estimated-cyto:57D11-57F8: 08/23/2001
Plate: RH.618 row: E column: 4
High quality sequence stop: 579.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   374 TCCGAGGACTGCCTTTTCCTTAATGTATATGCACCTAAAGTCAAAAGTACGCGGACTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   478 agcgactttgccgccttcaccaagcacacgggaaccaagatggtcgttgtaaatctccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              538 taccgtctcggcagctttggtttcctcgctggccaagccatgaaggactacggtgtaacg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             548 TACCGACTTGGAGCGCTTGGTTTCCTTAGTCTGCCCGAGGAGGAATACACGGNCATATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10; Length 676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 62; DB 10; Length 676
Pred. No. 0.7;
0; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="RH61852"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                                                                                                                BDGP/HHMI RH Drosophila EST Project
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/lab_host="DH5-alpha TonA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="male and female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lawrence Berkeley National Lab
                                                                         BI564550
BI564550.1 GI:15453742
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2001)
Contact: Stapleton, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 3.6%;
Best Local Similarity 54.6%;
Matches 172; Conservative
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                                                                                                                                         fruit fly.
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                                                                                             VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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                                                                            ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: Lambda Un1-ZAP XR, excised phagemid;
Site_1: ECORI; Site_2: XhoI; Seeds were surface-sterilized
, germinated and grown aseptically in the dark at room
temperature on filter paper with water, nystatin and
cefotaxime in covered crystallization dishes. Five-day
old seedlings were transferred to 5 cold room and kept
for 48 hr. The tissue, total RNA, and poly(A) RNA were
prepared, a cDNA library was made, and the cDNA clones
were in vivo excised to give pBluescript phagemids in the
TJ Close lab (Chol, Close, Fenton) at the University of
California, Riverside.
Sequencing were performed in the OD Anderson lab (all
                                                                                                Pacific
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RH61852.5prime RH Drosophila melanogaster normalized Head pFlc-1
    of the wheat
                                                                                                                                                                                                                                                                                                                                                                       /cultivara""Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE0359_B09_C17"
/clone=Ith="Wheat cold-stressed seedling cDNA library"
/dev_stage="Five-day old seedling"
/lab_host="E. coli_SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acgacacgatcagcgaccagtcgcagcgtctcccagttcgaccgcctcctcgccggcc 1195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 ACACCTACACCATCTCCTGGACGCCCTGCATGATCGTCTGGTACGTCGACGACGTCCCCA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 TCAGGGTGTTCCGCAACTACCGGGACAAGGGCATCGCGTACCCGATCAAGCGGCCCATGT 210
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                                                                              West Area, Western Regional Research Center 800 Buchman Street, Albany, CA 94710, USA 7e1: 5105595773
Fax: 5105595818
Email: oandersn@pw.usda.gov
Requence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: Strategene SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1256 acgegeegteaaagggeaacacettetegeateteggeegteateggaetegaeet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 ACGCCGTGGCAAGAAGGAGATGCAGTTCGTGCCTGGTTCGACCCCACCACCGACTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tegtetgecegacetactggacegegggegtteggetegteegeecacaagggeetet
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structure and function of the expressed portion omes - Cold-stressed seedling cDNA library
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Pred. No. 0.68;
0; Mismatches 180; Indels
                                                                                                                                                                                                                                                                                                                                                        /organism="Triticum aestivum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91
                                         Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture,
                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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other authors)
189 c 1
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1 (bases 1 to 730)

2 (bases 1 to 730)

3 Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Baxter, E., Berman, B., Carlson, J., Champe, M., Chavez, C., Chew, M., Dorsett, V., Farfan, J.D., Frise, E., George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G., Miranda, A., Misra, S., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., BDGP/HHMI AT Drosophila EST Project
Unpublished (2000)

On Dec 6, 2000 this sequence version replaced gi:11588396.
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//Organism="Drosophila melanogaster"
//Organism="taxon:7227"
//Olone_riff_taxon:7227"
//Clone_lib="AT Drosophila melanogaster adult testes pOTB7"
//Sex="male"
                                                                             PF505095
AT07260.5prime AT Drosophila melanogaster adult testes pOTB7
Drosophila melanogaster cDNA clone AT07260 5 similar to alpha-Est6:
FBan0001108 'enzyme' located on: 3R 8405-8405;: 04/07/2001, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 //dev_arage="0-3 day old ore-R males"
//lab_host="Plates AT.10-AT.120: DH5-alpha. Plates
//lab_host="Plates AT.10-AT.120: DH5-alpha. Plates
//lab_host="Plates AT.10-AT.120: DH5-alpha. Plates
//note="Organ: ADULT testes; Vector: porm3; Site_1: EcoRI;
Site_2: Xhol; The mRNA for the testis library was made
from testes and seminal vessicles hand dissected from 0-3
day old Ore-R males. RNA kindly provided by the lab of
Margaret Fuller. Sized fractionated cDNAs were directly
ligated into porm3? Plassmid cDNA library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic sequence AE003671
Plate: AT.72 row: E column: 12
High quality sequence stop: 601.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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Pred. No. 0.71;
0; Mismatches 135; Indels
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster
                                                                                                                                                                                                                                                BF505095.2 GI:13687701
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Best Local Similarity 53.0%;
Matches 159; Conservative
                                                                                                                                                                                            sequence.
BF505095
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Search completed: June 29, 2002, 13:05:40 Job time: 13711 sec

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